



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 178070**

**TO: Manjunath N Rao**  
**Location: rem/2A01/2C70**  
**Art Unit: 1652**  
**Tuesday, February 07, 2006**  
**Case Serial Number: 10/626583**

**From: Kristine Hensle**  
**Location: Biotech-Chem Library**  
**REM-1B69**  
**Phone: (571) 272-4161**

**Kristine. Hensle@uspto.gov**

### **Search Notes**

Examiner Rao,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Kristine Hensle  
Librarian  
STIC Biotech/Chem Library  
(571)272-4161

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178070 MEJ

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**STIC-Biotech/ChemLib**

**From:** Rao, Manjunath N.  
**Sent:** Tuesday, January 31, 2006 8:22 AM  
**To:** STIC-Biotech/ChemLib  
**Subject:** Sequence search request for 10626583

**From:** Manjunath N. Rao  
**Art Unit 1652, Room 2A01**  
**Mail Box in Room 2C70**  
**Phone:** 272-0939

RECEIVED  
JAN 31 2006  
STIC

**Date:** 1-31-06

Please search the following as soon as possible for application with serial number  
**10/626583**

1. **SEQ ID NO: 5** against all commercial amino acid sequence databases, issued patents/published applications amino acid sequence database and pending application amino acid sequence database. Please provide a print of results.

**If you have any questions please call me at the above phone number.**

Thanks

1/31/2006

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# STIC SEARCH RESULTS FEEDBACK FORM

## Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact:*

Mary Hale, Information Branch Supervisor  
Remsen Bldg. 01 D86  
571-272-2507

## Voluntary Results Feedback Form

➤ I am an examiner in Workgroup:  Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s).
- ☐ Non-Patent Literature  
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC Biotech-Chem Library, Remsen Bldg.



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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 3, 2006, 09:14:02 ; Search time 93 Seconds  
(without alignments)  
1006.319 Million cell updates/sec

Title: US-10-626-583-5

Perfect score: 1171

Sequence: 1 MFKKFKNFLVGLSAAALMSIS.....YQVMATEGYQSSGSNVTVW 213

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq 21.\*

- 1: geneseqp1980s.\*
- 2: geneseqp1990s.\*
- 3: geneseqp2000s.\*
- 4: geneseqp2001s.\*
- 5: geneseqp2002s.\*
- 6: geneseqp2003as.\*
- 7: geneseqp2003bs.\*
- 8: geneseqp2004s.\*
- 9: geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1171	100.0	213	3	Aay93752 A Bacteri
2	1171	100.0	213	7	Adc27541 Bacillus
3	1171	100.0	213	7	Ado55909 Bacillus
4	1171	100.0	213	8	Adj34972 Xylanase
5	1168	99.7	213	3	Aab48532 Bacillus
6	1168	99.7	213	3	Aab48518 Bacillus
7	1168	99.7	213	5	Aao18638 B subtili
8	1168	99.7	213	5	Aao18624 Endo-1,4-
9	1168	99.7	213	8	Adj35008 Xylanase
10	1168	99.7	213	8	Adi66728 B. circul
11	1168	99.7	213	8	Adi66740 B. subtil
12	1161	99.1	213	3	Aay93755 A bacteri
13	1154	98.5	213	3	Aay93753 A bacteri
14	1149	98.1	213	3	Aay93754 A bacteri
15	1130	96.5	213	2	Aar47200 Modified
16	1130	96.5	213	3	Aay93751 A bacteri
17	1125	96.1	213	8	Ado70164 Xylanase,
18	1104	94.3	213	8	Adj35014 Xylanase
19	1097	93.7	213	8	Adj35086 Xylanase
20	1041	88.9	185	2	Aaw60732 Xylanase
21	1041	88.9	185	3	Aay98064 B. subtil
22	1041	88.9	185	4	Aab69043 B. subtil
23	1041	88.9	185	4	Aau07391 Bacillus
24	1041	88.9	185	5	Aae18441 Bacillus

25	1041	88.9	185	7	Adc27530 Bacillus
26	1041	88.9	197	8	Adh10230 Xylanase
27	1041	88.9	353	4	Aab69045 Xylanase
28	1041	88.9	360	8	Adh10231 Xylanase
29	1038	88.6	185	2	Aaw60730 Xylanase
30	1038	88.6	185	3	Aay98062 B. circul
31	1038	88.6	185	5	Aao18625 B. circula
32	1038	88.6	185	5	Aae18439 Bacillus
33	1034	88.3	353	4	Aab69046 ND-xylana
34	1033	88.2	185	2	Aaw60279 Modified
35	1030	88.0	185	2	Aaw60278 Modified
36	987	84.3	185	3	Aab48524 Xylanase
37	987	84.3	185	3	Aab48523 Xylanase
38	987	84.3	185	5	Aao18629 Modified
39	987	84.3	185	5	Aao18630 Modified
40	987	84.3	185	8	Adi66732 B. circul
41	984	84.0	185	3	Aab48528 Xylanase
42	984	84.0	185	5	Aao18634 Modified
43	984	84.0	185	8	Adi66736 B. circul
44	979	83.6	185	3	Aab48526 Xylanase
45	979	83.6	185	5	Aao18632 Modified

#### ALIGNMENTS

##### RESULT 1

AAy93752  
ID AAY93752 standard; protein; 213 AA.  
XX  
AC AAY93752;  
XX  
DT 03-OCT-2000 (first entry)  
XX  
DE A bacterial endo-beta-1,4-xylanase protein.  
XX  
KW Endo-beta-1,4-xylanase inhibitor; wheat flour; xylanase; bakery product;  
KW dough; dough preparation.  
XX  
OS Bacillus subtilis.  
PN WO200039289-A2.  
XX  
PD 06-JUL-2000.  
XX  
PF 17-DEC-1999; 99WO-IB002071.  
XX  
PR 23-DEC-1998; 98GB-00028599.  
PR 06-APR-1999; 99GB-00007805.  
PR 15-APR-1999; 99GB-00008645.  
(DANI-) DANISCO AS.  
Sibbeesen O, Sorensen JF;  
WPI; 2000-465744/40.  
N-PSDB; AAA47154.  
Mutant xylanase protein identified using xylanase inhibitor useful for preparing non-sticky dough for bakery products.  
Claim 10; Page 108; 112pp; English.

The present sequence represents an endo-beta-1,4-xylanase. The specification also describes an endo-beta-1,4-xylanase inhibitor, which is obtained from wheat flour. The specification also describes a mutant xylanase protein. The xylanase is useful for preparing a foodstuff, preferably a bakery product or a substance (e.g. a dough) for making the bakery product. Wild type xylanase or mutant xylanase is useful for preparing a dough that is less sticky than a dough comprising a fungal xylanase. The xylanase inhibitor is useful for screening high degree resistance xylanases for dough preparation. The xylanase is also useful for preparing a non-sticky dough. A combination of xylanase and the

inhibitor is useful for calibrating and/or determining the quantity of inhibitor in a wheat flour sample

Sequence 213 AA;

Query Match 100.0%; Score 1171; DB 3; Length 213;  
Best Local Similarity 100.0%; Pred. No. 1.8e-91;  
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MFKEKKNFLVGLSAAALMSISLFSATASAASTDYQWNTDGGGINVAVNGSGGNTSVNWSN 60  
Db 1 MFKEKKNFLVGLSAAALMSISLFSATASAASTDYQWNTDGGGINVAVNGSGGNTSVNWSN 60  
Qy 61 TGNFVVGKGTGSPFRITINYNAGWAPNGNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTG 120  
Db 61 TGNFVVGKGTGSPFRITINYNAGWAPNGNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTG 120  
Qy 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGRTTFTQYWSVRSKRPTGSNATITFSNHVNA 180  
Db 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGRTTFTQYWSVRSKRPTGSNATITFSNHVNA 180  
Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213  
Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

#### RESULT 2

ADC27541  
ID ADC27541 standard; protein; 213 AA.  
XX  
AC ADC27541;  
DT 18-DEC-2003 (first entry)  
DE Bacillus subtilis wild-type xylanase enzyme.  
XX  
KW xylanase; xylanase inhibitor; thermosensitivity; plant cell wall;  
KW plant material; baking; processing cereal; starch production;  
KW processing wood; wood pulp bleaching; animal feed; flour separation;  
KW wetmilling; paper and pulp production; flour dough; hemicellulose;  
KW arabinoxylan; food supplement; xylan; baking process; bread volume;  
KW crumb structure; crumb appearance; shelf-life; enzyme.  
XX  
OS Bacillus subtilis.  
XX  
PN WO2003020923-A1.  
XX  
PD 13-MAR-2003.  
XX  
PF 30-AUG-2002; 2002WO-IB003797.  
XX  
PR 04-SEP-2001; 2001GB-00021387.  
XX  
PA (DANI-) DANISCO AS.  
XX  
PI Sibbesen O, Sorensen JF;  
XX  
XX WPI; 2003-332934/31.  
DR N-PSDB; ADC27538.  
XX  
PT Novel variant xylanase polypeptide having altered sensitivity to a  
PT xylanase inhibitor and altered thermosensitivity as compared with a  
PT parent xylanase enzyme, useful in baking, processing cereals, starch  
PT production.  
XX  
PS Disclosure; Fig 1; 63pp; English.  
XX  
CC This invention relates to a novel variant xylanase protein or its  
CC fragment having xylanase activity. The variants have one or more amino  
CC acid modifications so that the protein or fragment has an altered  
CC sensitivity to a xylanase inhibitor and has an altered thermosensitivity  
CC as compared with a parent xylanase enzyme. The variant xylanases of the  
CC invention are useful for degrading or modifying a plant cell wall, and

for processing a plant material. They may be useful for baking, processing cereals, starch production, in processing wood, and enhancing the bleaching of wood pulp. They may also be useful for a variety of applications such as animal feed, flour separation (wetmilling) and paper and pulp production. In addition, they may also be useful for preparing a flour dough. The enzymes of the invention may alter or reduce the viscosity derived from the presence of hemicellulose or arabinoxylan in a solution or system comprising plant cell wall material, and for modifying food and/or feed supplement comprising xylan. Use of the variant xylanases in baking processes improves the properties of flour based doughs and products made from the doughs. The baked products have highly desirable characteristics with respect to blood volume, crumb structure and appearance and additionally have an extended shelf-life. The enzymes of the invention have reduced thermosensitivity and inhibitor sensitivity, which allows a reduction in the amount of xylanase required for animal feed, starch production and baking. The present sequence is that of the full-length wild-type Bacillus subtilis xylanase which was used to create the variant xylanases of the invention.

Sequence 213 AA;

Query Match 100.0%; Score 1171; DB 7; Length 213;  
Best Local Similarity 100.0%; Pred. No. 1.8e-91;  
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKEKKNFLVGLSAAALMSISLFSATASAASTDYQWNTDGGGINVAVNGSGGNTSVNWSN 60  
Db 1 MFKEKKNFLVGLSAAALMSISLFSATASAASTDYQWNTDGGGINVAVNGSGGNTSVNWSN 60  
Qy 61 TGNFVVGKGTGSPFRITINYNAGWAPNGNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTG 120  
Db 61 TGNFVVGKGTGSPFRITINYNAGWAPNGNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTG 120  
Qy 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGRTTFTQYWSVRSKRPTGSNATITFSNHVNA 180  
Db 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGRTTFTQYWSVRSKRPTGSNATITFSNHVNA 180  
Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213  
Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

#### RESULT 3

ADO55909  
ID ADO55909 standard; protein; 213 AA.  
XX  
AC ADO55909;  
XX  
DT 15-JUL-2004 (first entry)  
XX  
DE Bacillus subtilis xynA protein sequence SeqID4.  
XX  
KW cellulase; microorganism; organic fertilizer; faeces; urine;  
KW domestic animal; sawdust; pLYH7-39; bglc; xylanase; pLYH8-49; xynA;  
KW pLYH8-62; xynD; pectate lyase; pLYH9-24; pella; pLYH9-46; pella;  
KW fermentation; enzyme.  
XX  
OS Bacillus subtilis.  
XX  
PN KR2003015943-A.  
XX  
PD 26-FEB-2003.  
XX  
PF 18-AUG-2001; 2001KR-00049794.  
XX  
PR 18-AUG-2001; 2001KR-00049794.  
XX  
PA (KOBI-) KOREA BIO FERTILIZER CO LTD.  
XX  
PI Lee YH, Yoon HJ;  
XX  
DR WPI; 2003-455433/43.  
DR N-PSDB; ADO55908.



XX Gene encoding cellulase, cellulase expressed by the same, microorganism  
 PT containing the same gene, and organic fertilizer using the same  
 PT microorganism.  
 XX  
 PS Claim 2; SEQ ID NO 4; 1pp; Korean.  
 XX  
 CC This invention relates to novel genes encoding cellulase, cellulase  
 CC expressed by the same, a microorganism containing the same gene, and an  
 CC organic fertilizer using the same microorganism, therefore the organic  
 CC fertilizer can be rapidly produced from a mixture of the faeces and urine  
 CC of domestic animals and sawdust. The microorganism *Bacillus subtilis*  
 CC contains one cellulase encoding gene pLVH7-39(bglC), two xylanase  
 CC encoding genes pLVH8-49(xyNA) and pLVH8-62(xyNB) and two pectate lyase  
 CC encoding genes pLVH9-24(peiA) and pLVH9-46(peiB). The organic fertilizer  
 CC is produced by inoculating an appropriate amount of the microorganism  
 CC *Bacillus subtilis* into the mixture of the faeces and urine of domestic  
 CC animals and sawdust and fermenting the mixture. The present sequence is  
 CC that of a *Bacillus subtilis* protein which is related to the production of  
 CC the organic fertilizer of the invention.

XX Sequence 213 AA;

Query Match 100.0%; Score 1171; DB 7; Length 213;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-91;  
 Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MFKPKNPLVGLSALMSISLFSATASASTDYQWNTDGGGVNNAVNGSGNYSVNWSN 60  
 Db 1 MFKPKNPLVGLSALMSISLFSATASASTDYQWNTDGGGVNNAVNGSGNYSVNWSN 60  
 Qy 61 TGNFVVGKGTGSPFRITINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGYRPTG 120  
 Db 61 TGNFVVGKGTGSPFRITINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGYRPTG 120  
 Qy 121 TYGTVKSDGGTYDIYTTTTRYNAPSIDGDRITFTQYWSVRSKRPTGNSNATITFSNHVNA 180  
 Db 121 TYGTVKSDGGTYDIYTTTTRYNAPSIDGDRITFTQYWSVRSKRPTGNSNATITFSNHVNA 180  
 Qy 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213  
 Db 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213

RESULT 4

ADJ34972  
 ID ADJ34972 standard; protein; 213 AA.

XX ADJ34972;

XX 22-APR-2004 (first entry)

XX Xylanase from an environmental sample seq id 188.

XX antibacterial; fungicide; thermostable xylanase activity;  
 KW dough conditioning; beverage production; nutritional supplement;  
 KW animal feed; lignin reduction; wood product; xylan; bacterial infection;  
 KW fungal infection; coccidiosis.

XX Unidentified.

XX WO2003106654-A2.

XX 24-DEC-2003.

XX 16-JUN-2003; 2003WO-US019153.

XX 14-JUN-2002; 2002US-0389299P.

XX (DIVE-) DIVERSA CORP.

XX Steer B, Callen W, Healey S, Hazlewood G, Wu D, Blum D;  
 PI Esteghlalian A;

PI

XX

DR WPI; 2004-099016/10.  
 DR N-PSDB; ADJ34971.

XX Novel xylanase recombinant polypeptide useful for improving textile  
 PT texture, treating paper, eliminating microorganisms.

XX Claim 60; SEQ ID NO 188; 570pp; English.

XX The invention describes an isolated or recombinant polypeptide (I),  
 CC having 50% or more identity to 190 300-1200 residue amino acid sequences  
 CC (SI), given in the specification, over a region of 100 or more residues  
 CC and the polypeptide as thermostable xylanase activity. (I) is useful for:  
 CC dough conditioning; beverage production; as a nutritional supplement in  
 CC animal feed; reducing lignin in a wood or a wood product; and for  
 CC eliminating and protecting animals from a microorganism comprising xylan.  
 CC The polynucleotide (II) encoding (I) is useful for amplifying nucleic  
 CC acid encoding a polypeptide having a xylanase activity which involves  
 CC amplification of a template nucleic acid with a primer pair capable of  
 CC amplifying (II) or its subsequence. (I) is useful for treating and  
 CC preventing bacterial infection and fungal infection e.g. coccidiosis.  
 CC This is the amino acid sequence of a xylanase protein isolated from an  
 CC environmental sample.

XX Sequence 213 AA;

Query Match 100.0%; Score 1171; DB 8; Length 213;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-91;  
 Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MFKPKNPLVGLSALMSISLFSATASASTDYQWNTDGGGVNNAVNGSGNYSVNWSN 60  
 Db 1 MFKPKNPLVGLSALMSISLFSATASASTDYQWNTDGGGVNNAVNGSGNYSVNWSN 60  
 Qy 61 TGNFVVGKGTGSPFRITINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGYRPTG 120  
 Db 61 TGNFVVGKGTGSPFRITINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVDSWGYRPTG 120  
 Qy 121 TYGTVKSDGGTYDIYTTTTRYNAPSIDGDRITFTQYWSVRSKRPTGNSNATITFSNHVNA 180  
 Db 121 TYGTVKSDGGTYDIYTTTTRYNAPSIDGDRITFTQYWSVRSKRPTGNSNATITFSNHVNA 180  
 Qy 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213  
 Db 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213

RESULT 5

AAB48532

ID AAB48532 standard; protein; 213 AA.

XX AAB48532;

XX 05-MAR-2001 (first entry)

XX *Bacillus subtilis* xylanase.

XX Bacterial; *Bacillus circulans*; xylanase; xylanase activity; XA;  
 KW bleaching agent.

XX *Bacillus subtilis*.

XX WO200068396-A2.

XX 16-NOV-2000.

XX 12-MAY-2000; 2000WO-US013172.

XX 12-MAY-1999; 99US-0133714P.

XX (XENC-) XENCOR INC.

XX Bentzien JM;

XX WPI; 2000-679800/66.  
XX Non naturally occurring XA protein with enhanced thermophilicity,  
PT alkalophilicity or thermostability relative to the naturally occurring  
PT Bacillus circulans xylanase is used in an agent for bleaching pulp.  
XX  
XX  
PS Disclosure; Fig 16A; 114pp; English.  
XX  
CC The present sequence is given in a specification relating to non  
CC naturally occurring xylanase activity (XA) proteins. The XA proteins  
CC comprise an amino acid sequence less than 97% identical to a naturally  
CC occurring Bacillus circulans xylanase. They are modified to exhibit  
CC enhanced thermophilicity, alkalophilicity or thermostability relative to  
CC the naturally occurring B. circulans xylanase. They may be used as the  
CC active compound in a bleaching agent which is used for bleaching pulp  
XX  
SQ Sequence 213 AA;  
  
Query Match 99.7%; Score 1168; DB 3; Length 213;  
Best Local Similarity 99.5%; Pred. No. 3.3e-91;  
Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MFKEKKNFLVGLSAAALMSISLFSATASAASTDYQWNTDGGGIYNAVNGSGGYSVNWNSN 60  
Db 1 MFKEKKNFLVGLSAAALMSISLFSATASAASTDYQWNTDGGGIYNAVNGSGGYSVNWNSN 60  
  
Qy 61 TGNFVVGKGMTTGSPPFTINYNAGVWAPNGNGYLTLXGWTSPLEIYYVVDSWGTYRPTG 120  
Db 61 TGNFVVGKGMTTGSPPFTINYNAGVWAPNGNGYLTLXGWTSPLEIYYVVDSWGTYRPTG 120  
  
Qy 121 TYKGTVKS DGGTYDIYTTTRYNAPSIDGDRITFTQYMSVRSQSKRPTGSNATITFSNHVNA 180  
Db 121 TYKGTVKS DGGTYDIYTTTRYNAPSIDGDRITFTQYMSVRSQSKRPTGSNATITFSNHVNA 180  
  
Qy 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVM 213  
Db 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVM 213  
  
RESULT 6  
AAB48518  
ID AAB48518 standard; protein; 213 AA.  
XX  
AC AAB48518;  
XX  
DT 05-MAR-2001 (first entry)  
XX  
DE Bacillus circulans endo-1,4-beta xylanase precursor.  
XX  
KW Bacillus circulans; xylanase; xylanase activity; XA; bleaching agent.  
XX  
OS Bacillus circulans.  
XX  
PN WO200068396-A2.  
XX  
PD 16-NOV-2000.  
XX  
PF 12-MAY-2000; 2000WO-US013172.  
XX  
PR 12-MAY-1999; 99US-0133714P.  
XX  
PA (XENC-) XENCOR INC.  
XX  
PI Bentzien JM;  
XX  
DR WPI; 2000-679800/66.  
XX  
CC Non naturally occurring XA protein with enhanced thermophilicity,  
XX alkalophilicity or thermostability relative to the naturally occurring  
PT Bacillus circulans xylanase is used in an agent for bleaching pulp.  
XX  
XX Disclosure; Fig 1A; 114pp; English.

XX The present sequence is given in a specification relating to non  
CC naturally occurring xylanase activity (XA) proteins. The XA proteins  
CC comprise an amino acid sequence less than 97% identical to a naturally  
CC occurring Bacillus circulans xylanase. They are modified to exhibit  
CC enhanced thermophilicity, alkalophilicity or thermostability relative to  
CC the naturally occurring B. circulans xylanase. They may be used as the  
CC active compound in a bleaching agent which is used for bleaching pulp  
XX  
SQ Sequence 213 AA;  
  
Query Match 99.7%; Score 1168; DB 3; Length 213;  
Best Local Similarity 99.5%; Pred. No. 3.3e-91;  
Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MFKEKKNFLVGLSAAALMSISLFSATASAASTDYQWNTDGGGIYNAVNGSGGYSVNWNSN 60  
Db 1 MFKEKKNFLVGLSAAALMSISLFSATASAASTDYQWNTDGGGIYNAVNGSGGYSVNWNSN 60  
  
Qy 61 TGNFVVGKGMTTGSPPFTINYNAGVWAPNGNGYLTLXGWTSPLEIYYVVDSWGTYRPTG 120  
Db 61 TGNFVVGKGMTTGSPPFTINYNAGVWAPNGNGYLTLXGWTSPLEIYYVVDSWGTYRPTG 120  
  
Qy 121 TYKGTVKS DGGTYDIYTTTRYNAPSIDGDRITFTQYMSVRSQSKRPTGSNATITFSNHVNA 180  
Db 121 TYKGTVKS DGGTYDIYTTTRYNAPSIDGDRITFTQYMSVRSQSKRPTGSNATITFSNHVNA 180  
  
Qy 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVM 213  
Db 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVM 213  
  
RESULT 7  
AAO18638  
ID AAO18638 standard; protein; 213 AA.  
XX  
AC AAO18638;  
XX  
DT 24-OCT-2002 (first entry)  
XX  
DE B subtilis xylanase.  
XX  
KW Xylanase activity; enzyme; thermostable; xylanase; pulp bleaching;  
KW liquid clarification; coffee extraction; plant oil extraction;  
KW starch extraction; food thickener; animal food additive; mutant; muten.  
XX  
OS Bacillus subtilis.  
XX  
PN WO200238746-A2.  
XX  
PD 16-MAY-2002.  
XX  
PF 09-NOV-2001; 2001WO-US048018.  
XX  
PR 10-NOV-2000; 2000US-00710050.  
XX  
PA (XENC-) XENCOR INC.  
XX  
PI Bentzien J, Dahiyat B;  
XX  
DR WPI; 2002-608200/65.  
XX  
PT Novel xylanase activity protein, useful in bleaching process of pulp and  
PT in food and animal feed industry, has enhanced thermostability and  
PT alkalophilicity.  
XX  
PS Disclosure; Fig 16A; 121pp; English.  
XX  
CC The present invention relates to a non-naturally occurring xylanase  
CC activity (XA) protein comprising an amino acid sequence less than 97%  
CC identical to a naturally occurring Bacillus circulans xylanase, where the  
CC protein has been modified to exhibit enhanced thermophilicity,  
CC alkalophilicity, or thermostability relative to naturally occurring B.

CC circulans xylanase, and has at least 5 amino acid substitutions. A  
CC bleaching agent comprising a modified xylanase is useful for bleaching  
CC pulp, in the bioconversion of lignocellulosic materials to fuels, for  
CC clarifying juice and wine, extracting coffee, plant oils and starch,  
CC producing food thickeners, altering texture in bakery products, e.g.  
CC improving the quality of dough, helping bread to rise and processing of  
CC wheat and corn for starch production, use as animal food additives to aid  
CC in the digestibility of feedstuffs and in the washing of super precision  
CC devices and semiconductors. The present sequence is a xylanase protein  
CC described in the exemplification of the invention  
XX  
SQ Sequence 213 AA;

Query Match 99.7%; Score 1168; DB 5; Length 213;  
Best Local Similarity 99.5%; Pred. No. 3.3e-91;  
Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MFKEKKNFLVGLSAAALMSISLFSATASAASTDYQWNTDGGIYVNAVNGSGNYSVNWSN 60  
DB 1 MFKEKKNFLVGLSAAALMSISLFSATASAASTDYQWNTDGGIYVNAVNGSGNYSVNWSN 60  
QY 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLYLTYGWTSPLEIYYVVDVDSWGTYRPTG 120  
DB 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLYLTYGWTSPLEIYYVVDVDSWGTYRPTG 120  
QY 121 TYKGTVKSDDGTYYITTYTRYNAPSIDGDRITFTQYWSVRSQKPTGSGNATITFSNHVNA 180  
DB 121 TYKGTVKSDDGTYYITTYTRYNAPSIDGDRITFTQYWSVRSQKPTGSGNATITFSNHVNA 180  
QY 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213  
DB 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213

RESULT 8  
AAO18624  
ID AAO18624 standard; protein; 213 AA.  
XX AAO18624;  
AC  
XX  
DT 24-OCT-2002 (first entry)  
XX  
DE Endo-1,4-beta xylanase precursor protein.  
XX  
Xylanase activity; enzyme; thermostable; xylanase; pulp bleaching;  
KW liquid clarification; coffee extraction; plant oil extraction;  
KW starch extraction; food thickener; animal food additive; mutant; mutein.  
XX  
OS Unidentified.  
XX  
PN WO200238746-A2.  
XX  
PD 16-MAY-2002.  
XX  
PF 09-NOV-2001; 2001WO-US048018.  
XX  
PR 10-NOV-2000; 2000US-00710050.  
XX  
PA (XENC-) XENCOR INC.  
XX  
PI Bentzien J, Dahiyat B;  
XX  
WPI; 2002-608200/65.  
XX  
Novel xylanase activity protein, useful in bleaching process of pulp and  
PT in food and animal feed industry, has enhanced thermostability and  
PT alkalophilicity.  
XX  
PS Disclosure; Fig 1A; 121pp; English.  
XX  
The present invention relates to a non-naturally occurring xylanase  
CC activity (XA) protein comprising an amino acid sequence less than 97%  
CC identical to a naturally occurring Bacillus circulans xylanase, where the

CC protein has been modified to exhibit enhanced thermophilicity,  
CC alkalophilicity, or thermostability relative to naturally occurring B.  
CC circulans xylanase, and has at least 5 amino acid substitutions. A  
CC bleaching agent comprising a modified xylanase is useful for bleaching  
CC pulp, in the bioconversion of lignocellulosic materials to fuels, for  
CC clarifying juice and wine, extracting coffee, plant oils and starch,  
CC producing food thickeners, altering texture in bakery products, e.g.  
CC improving the quality of dough, helping bread to rise and processing of  
CC wheat and corn for starch production, use as animal food additives to aid  
CC in the digestibility of feedstuffs and in the washing of super precision  
CC devices and semiconductors. The present sequence is a xylanase protein  
CC described in the exemplification of the invention  
XX  
SQ Sequence 213 AA;

Query Match 99.7%; Score 1168; DB 5; Length 213;  
Best Local Similarity 99.5%; Pred. No. 3.3e-91;  
Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MFKEKKNFLVGLSAAALMSISLFSATASAASTDYQWNTDGGIYVNAVNGSGNYSVNWSN 60  
DB 1 MFKEKKNFLVGLSAAALMSISLFSATASAASTDYQWNTDGGIYVNAVNGSGNYSVNWSN 60  
QY 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLYLTYGWTSPLEIYYVVDVDSWGTYRPTG 120  
DB 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLYLTYGWTSPLEIYYVVDVDSWGTYRPTG 120  
QY 121 TYKGTVKSDDGTYYITTYTRYNAPSIDGDRITFTQYWSVRSQKPTGSGNATITFSNHVNA 180  
DB 121 TYKGTVKSDDGTYYITTYTRYNAPSIDGDRITFTQYWSVRSQKPTGSGNATITFSNHVNA 180  
QY 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213  
DB 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213

RESULT 9  
ADJ35008  
ID ADJ35008 standard; protein; 213 AA.  
XX ADJ35008;  
AC  
XX  
DT 22-APR-2004 (first entry)  
XX  
Xylanase from an environmental sample seq id 224.  
DE  
XX  
antibacterial; fungicide; thermostable xylanase activity;  
KW dough conditioning; beverage production; nutritional supplement;  
KW animal feed; lignin reduction; wood product; xylan; bacterial infection;  
KW fungal infection; coccidioidosis.  
XX  
OS Unidentified.  
XX  
PN WO2003106654-A2.  
XX  
PD 24-DEC-2003.  
XX  
PF 16-JUN-2003; 2003WO-US019153.  
XX  
PR 14-JUN-2002; 2002US-0389299P.  
XX  
PA (DIVE-) DIVERSA CORP.  
XX  
PI Steer B, Callen W, Healey S, Hazlewood G, Wu D, Blum D;  
PI Esteghlalian A;  
XX  
WPI; 2004-099016/10.  
DR N-PSDB; ADJ35007.  
XX  
Novel xylanase recombinant polypeptide useful for improving textile  
PT texture, treating paper, eliminating microorganisms.  
XX  
Claim 60; SEQ ID NO 224; 570pp; English.

XX The invention describes an isolated or recombinant polypeptide (I),  
 CC having 50% or more identity to 190-1200 residue amino acid sequences  
 CC (S1), given in the specification, over a region of 100 or more residues  
 CC and the polypeptide as thermostable xylanase activity. (I) is useful for:  
 CC dough conditioning; beverage production; as a nutritional supplement in  
 CC animal feed; reducing lignin in a wood or a wood product; and for  
 CC eliminating and protecting animals from a microorganism comprising xylan.  
 CC The polynucleotide (II) encoding (I) is useful for amplifying nucleic  
 CC acid encoding a polypeptide having a xylanase activity which involves  
 CC amplification of a template nucleic acid with a primer pair capable of  
 CC amplifying (II) or its subsequence. (I) is useful for treating and  
 CC preventing bacterial infection and fungal infection e.g. coccidiosis.  
 CC This is the amino acid sequence of a xylanase protein isolated from an  
 CC environmental sample.  
 XX  
 SQ Sequence 213 AA;

Query Match 99.7%; Score 1168; DB 8; Length 213;  
 Best Local Similarity 99.5%; Pred. No. 3.3e-91;  
 Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MFKPKNPLVGLSALMSISLFSATASASTDYQNWTDGGGIYNAVNGSGNYVNWNSN 60  
 Db 1 MFKPKNPLVGLSALMSISLFSATASASTDYQNWTDGGGIYNAVNGSGNYVNWNSN 60  
 Qy 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLLYGWTRSPLEIYYVVDWSGTYRPTG 120  
 Db 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLLYGWTRSPLEIYYVVDWSGTYRPTG 120  
 Qy 121 TYKGTVKS DGGTYDIYTTTTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVNA 180  
 Db 121 TYKGTVKS DGGTYDIYTTTTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVNA 180  
 Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213  
 Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

RESULT 10  
 ADI66728  
 ID ADI66728 standard; protein; 213 AA.  
 XX  
 AC ADI66728;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE B. circulans endo-1,4-beta xylanase.  
 XX  
 KW Endo-1,4-beta xylanase; XA; EC 3.2.1.8; enzyme; bleaching;  
 KW bleaching pulp; paper industry; food; animal feed; thermostability;  
 KW alkalophilic; hot alkali treatment.  
 XX  
 OS Bacillus circulans.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..28  
 FT /note= "Signal peptide"  
 FT Protein 29..213  
 FT /note= "Mature Xylanase"  
 XX  
 US6682923-B1.  
 XX  
 XX 27-JAN-2004.  
 XX  
 PF 12-MAY-2000; 2000US-00570856.  
 XX  
 PR 12-MAY-1999; 99US-0133714P.  
 PR 07-JUN-1999; 99US-0138156P.  
 XX  
 PA (XENC-) XENCOR.  
 XX  
 PI Bentzien J, Dahiyat BI;

XX WPI; 2004-118575/12.  
 DR N-PSDB; ADI66729.  
 XX  
 PT New mutant xylanase (XA) protein comprising at least four amino acid  
 FT substitutions as compared to Bacillus circulans xylanase, useful for  
 PT bleaching (paper) pulp, and in the food and animal feed industries.  
 XX  
 PS Claim 2; SEQ ID NO 1; 84pp; English.  
 XX  
 CC The invention relates to a mutant xylanase activity (XA, endo-1,4-beta  
 CC xylanase from Bacillus circulans) protein appearing as ADI66730. Also  
 CC included is a bleaching agent comprising the XA protein. The non-  
 CC naturally occurring XA protein comprises at least four amino acid  
 CC substitutions as compared to Bacillus circulans xylanase ADI66728. The  
 CC amino acid substitutions are made at positions 26, 28, 30, 53, 58, 64,  
 CC 79, 105, 142, 144, 171, 176, 180 or 182, especially at positions 28, 30,  
 CC 58, or 144. The non-naturally occurring xylanase activity (XA) protein is  
 CC useful for bleaching pulp in the paper and related industries, but is  
 CC also useful in the food and animal feed industries. The new protein is  
 CC active at higher pH and temperature ranges than naturally occurring  
 CC xylanases, simplifying incorporation of the xylanase treatment step into  
 CC pulp processing, especially where the enzyme is added after hot alkali  
 CC treatment. The present sequence represents the wild-type xylanase.  
 XX  
 SQ Sequence 213 AA;  
 Query Match 99.7%; Score 1168; DB 8; Length 213;  
 Best Local Similarity 99.5%; Pred. No. 3.3e-91;  
 Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MFKPKNPLVGLSALMSISLFSATASASTDYQNWTDGGGIYNAVNGSGNYVNWNSN 60  
 Db 1 MFKPKNPLVGLSALMSISLFSATASASTDYQNWTDGGGIYNAVNGSGNYVNWNSN 60  
 Qy 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLLYGWTRSPLEIYYVVDWSGTYRPTG 120  
 Db 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLLYGWTRSPLEIYYVVDWSGTYRPTG 120  
 Qy 121 TYKGTVKS DGGTYDIYTTTTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVNA 180  
 Db 121 TYKGTVKS DGGTYDIYTTTTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVNA 180  
 Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213  
 Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213  
 RESULT 11  
 ADI66740  
 ID ADI66740 standard; protein; 213 AA.  
 XX  
 AC ADI66740;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE B. subtilis xylanase.  
 XX  
 KW Xylanase; XA; EC 3.2.1.8; enzyme; bleaching; bleaching pulp;  
 KW paper industry; food; animal feed; thermostability; alkalophilic;  
 KW hot alkali treatment.  
 XX  
 OS Bacillus subtilis.  
 XX  
 XX US6682923-B1.  
 XX  
 XX 27-JAN-2004.  
 XX  
 PF 12-MAY-2000; 2000US-00570856.  
 XX  
 PR 12-MAY-1999; 99US-0133714P.  
 PR 07-JUN-1999; 99US-0138156P.  
 XX  
 PA (XENC-) XENCOR.  
 XX  
 PI Bentzien J, Dahiyat BI;

(XENC-) XENCOR.  
PA XX  
XX XX  
PI Bentzien J, Dahiyat BI;  
XX XX  
DR WPI; 2004-118575/12.  
XX XX  
XX New mutant xylanase (XA) protein comprising at least four amino acid  
XX PT substitutions as compared to Bacillus circulans xylanase, useful for  
XX PT bleaching (paper) pulp, and in the food and animal feed industries.  
XX XX  
XX Disclosure; SEQ ID NO 13; 84pp; English.  
XX XX  
XX The invention relates to a mutant xylanase activity (XA, endo-1,4-beta  
XX CC xylanase from Bacillus circulans) protein appearing as ADI66730. Also  
XX CC included is a bleaching agent comprising the XA protein. The non-  
XX CC naturally occurring XA protein comprises at least four amino acid  
XX CC substitutions as compared to Bacillus circulans xylanase ADI66728. The  
XX CC amino acid substitutions are made at positions 26, 28, 30, 53, 58, 64,  
XX CC 79, 105, 142, 144, 171, 176, 180 or 182, especially at positions 28, 30,  
XX CC 58, or 144. The non-naturally occurring xylanase activity (XA) protein is  
XX CC useful for bleaching pulp in the paper and related industries, but is  
XX CC also useful in the food and animal feed industries. The new protein is  
XX CC active at higher pH and temperature ranges than naturally occurring  
XX CC xylanases, simplifying incorporation of the xylanase treatment step into  
XX CC pulp processing, especially where the enzyme is added after hot alkali  
XX CC treatment. The present sequence is a xylanase from another species  
XX CC included for comparison.  
XX XX  
SQ Sequence 213 AA;  
Query Match 99.7%; Score 1168; DB 8; Length 213;  
Best Local Similarity 99.5%; Pred. No. 3.3e-91; Mismatches 0; Indels 0; Gaps 0;  
Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MFKEKQFLVGLSAAALMSISLFSATASAASTDYQNWNTDGGGIYNAVNGSGGYSVNVWSN 60  
DB 1 MFKEKQFLVGLSAAALMSISLFSATASAASTDYQNWNTDGGGIYNAVNGSGGYSVNVWSN 60  
QY 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLTLYGWTSPLEIYYVVDVDSWGTYPRTG 120  
DB 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLTLYGWTSPLEIYYVVDVDSWGTYPRTG 120  
QY 121 TYKGTVKS DGGTYDIYTTTRYNAPSIDGDRFTTQYWSVRSQSKPTGSNATITFSNVNA 180  
DB 121 TYKGTVKS DGGTYDIYTTTRYNAPSIDGDRFTTQYWSVRSQSKPTGSNATITFSNVNA 180  
QY 181 WKSHGMGLSNWAYQVWATEGYQSSGSSNVTVW 213  
DB 181 WKSHGMGLSNWAYQVWATEGYQSSGSSNVTVW 213  
RESULT 12  
AAAY93755  
ID AAY93755 standard; protein; 213 AA.  
XX  
AC AAY93755;  
XX  
DT 03-OCT-2000 (first entry)  
XX  
XX A bacterial endo-beta-1,4-xylanase mutant XM3.  
XX  
XX Endo-beta-1,4-xylanase inhibitor; wheat flour; xylanase; bakery product;  
XX KW dough; dough preparation.  
XX  
XX Synthetic.  
XX OS Bacillus subtilis.  
XX FN WO200039289-A2.  
XX  
XX PD 06-JUL-2000.  
XX  
XX PF 17-DEC-1999; 99WO-IB002071.  
XX  
XX  
PR 23-DEC-1998; 98GB-00028599.  
PR 06-APR-1999; 99GB-00007805.  
PR 15-APR-1999; 99GB-00008645.  
XX  
XX (DANI-) DANISCO AS.  
XX PA  
XX Sibbesen O, Sorensen JF;  
PI  
XX WPI; 2000-465744/40.  
DR N-PSDB; AAA47157.  
XX  
XX Mutant xylanase protein identified using xylanase inhibitor useful for  
XX PT preparing non-sticky dough for bakery products.  
XX  
XX Claim 1; Page 111; 112pp; English.  
XX  
XX The present sequence represents a mutant endo-beta-1,4-xylanase. The  
XX CC specification also describes an endo-beta-1,4-xylanase inhibitor, which  
XX CC is obtained from wheat flour. The specification also describes a mutant  
XX CC xylanase protein. The xylanase is useful for preparing a foodstuff.  
XX CC preferably a bakery product or a substance (e.g. a dough) for making the  
XX CC bakery product. Wild type xylanase or mutant xylanase is useful for  
XX CC preparing a dough that is less sticky than a dough comprising a fungal  
XX CC xylanase. The xylanase inhibitor is useful for screening high degree  
XX CC resistance xylanases for dough preparation. The xylanase is also useful  
XX CC for preparing a non-sticky dough. A combination of xylanase and the  
XX CC inhibitor is useful for calibrating and/or determining the quantity of  
XX CC inhibitor in a wheat flour sample  
XX XX  
SQ Sequence 213 AA;  
Query Match 99.1%; Score 1161; DB 3; Length 213;  
Best Local Similarity 99.1%; Pred. No. 1.3e-90; Mismatches 2; Indels 0; Gaps 0;  
Matches 211; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MFKEKQFLVGLSAAALMSISLFSATASAASTDYQNWNTDGGGIYNAVNGSGGYSVNVWSN 60  
DB 1 MFKEKQFLVGLSAAALMSISLFSATASAASTDYQNWNTDGGGIYNAVNGSGGYSVNVWSN 60  
QY 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLTLYGWTSPLEIYYVVDVDSWGTYPRTG 120  
DB 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLTLYGWTSPLEIYYVVDVDSWGTYPRTG 120  
QY 121 TYKGTVKS DGGTYDIYTTTRYNAPSIDGDRFTTQYWSVRSQSKPTGSNATITFSNVNA 180  
DB 121 TYKGTVKS DGGTYDIYTTTRYNAPSIDGDRFTTQYWSVRSQSKPTGSNATITFSNVNA 180  
QY 181 WKSHGMGLSNWAYQVWATEGYQSSGSSNVTVW 213  
DB 181 WKSHGMGLSNWAYQVWATEGYQSSGSSNVTVW 213  
RESULT 13  
AAAY93753  
ID AAY93753 standard; protein; 213 AA.  
XX  
AC AAY93753;  
XX  
DT 03-OCT-2000 (first entry)  
XX  
XX A bacterial endo-beta-1,4-xylanase mutant XM1.  
XX  
XX Endo-beta-1,4-xylanase inhibitor; wheat flour; xylanase; bakery product;  
XX KW dough; dough preparation.  
XX  
XX Synthetic.  
XX OS Bacillus subtilis.  
XX  
XX Key Location/Qualifiers  
XX FH Misc-difference 43  
XX FT Misc-difference 197 /note= "wild type Ile changed to Thr"  
XX FT Misc-difference 197 /note= "wild type Met changed to Leu"

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FT Misc-difference 203
FT /note= "wild type Gln changed to Lys"
XX OS Synthetic.
XX OS Bacillus subtilis.
XX PN WO200039289-A2.
XX XX
XX PD 06-JUL-2000.
XX XX
XX PF 17-DEC-1999; 99WO-IB002071.
XX XX
XX PR 23-DEC-1998; 98GB-00028599.
XX PR 06-APR-1999; 99GB-00007805.
XX PR 15-APR-1999; 99GB-00008645.
XX XX
XX PA (DANI-) DANISCO AS.
XX XX
XX PI Sibbesen O, Sorensen JF;
XX XX
XX DR WPI; 2000-465744/40.
XX DR N-PSDB; AAA47156.
XX XX
XX PT Mutant xylanase protein identified using xylanase inhibitor useful for
XX PT preparing non-sticky dough for bakery products.
XX PS Claim 1; Page 109; 112pp; English.
XX XX
XX CC The present sequence represents a mutant endo-beta-1,4-xylanase. The
XX CC specification also describes an endo-beta-1,4-xylanase inhibitor, which
XX CC is obtained from wheat flour. The specification also describes a mutant
XX CC xylanase protein. The xylanase is useful for preparing a foodstuff.
XX CC preferably a bakery product or a substance (e.g. a dough) for making the
XX CC bakery product. Wild type xylanase or mutant xylanase is useful for
XX CC preparing a dough that is less sticky than a dough comprising a fungal
XX CC xylanase. The xylanase inhibitor is useful for screening high degree
XX CC resistance xylanases for dough preparation. The xylanase is also useful
XX CC for preparing a non-sticky dough. A combination of xylanase and the
XX CC inhibitor is useful for calibrating and/or determining the quantity of
XX CC inhibitor in a wheat flour sample
XX XX
SQ Sequence 213 AA;
Query Match 98.1%; Score 1154; DB 3; Length 213;
Best Local Similarity 98.1%; Pred. No. 5.1e-90;
Matches 209; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MFKFKNFLVGLSAAALMSISLFSATASAASTDYQNNWTDGGGIYNAVNGSGGNTSVNWSN 60
Db 1 MFKFKNFLVGLSAAALMSISLFSATASAASTDYQNNWTDGGGTNAVNGSGGNTSVNWSN 60
Qy 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLLTYGWTSPLEIYYVVDWSGTYRPTG 120
Db 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLLTYGWTSPLEIYYVVDWSGTYRPTG 120
Qy 121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRFTFTQYWSVRSKRPTGSNATITFSNHVNA 180
Db 121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRFTFTQYWSVRSKRPTGSNATITFSNHVNA 180
Qy 181 WKSHGMNLGSNWAYQVWMATEGYQSSGSSNTVTW 213
Db 181 WKSHGMNLGSNWAYQVWMATEGYKSSGSSNTVTW 213
RESULT 14
AAY93754
ID AAY93754 standard; protein; 213 AA.
XX XX
XX AC AAY93754;
XX XX
XX DT 03-OCT-2000 (first entry)
XX XX
XX DE A bacterial endo-beta-1,4-xylanase mutant XM2.
XX XX
XX KW Endo-beta-1,4-xylanase inhibitor; wheat flour; xylanase; bakery product;
XX KW dough; dough preparation.

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XX OS Synthetic.
XX OS Bacillus subtilis.
XX PN WO200039289-A2.
XX XX
XX PD 06-JUL-2000.
XX XX
XX PF 17-DEC-1999; 99WO-IB002071.
XX XX
XX PR 23-DEC-1998; 98GB-00028599.
XX PR 06-APR-1999; 99GB-00007805.
XX PR 15-APR-1999; 99GB-00008645.
XX XX
XX PA (DANI-) DANISCO AS.
XX XX
XX PI Sibbesen O, Sorensen JF;
XX XX
XX DR WPI; 2000-465744/40.
XX DR N-PSDB; AAA47156.
XX XX
XX PT Mutant xylanase protein identified using xylanase inhibitor useful for
XX PT preparing non-sticky dough for bakery products.
XX PS Claim 1; Page 110; 112pp; English.
XX XX
XX CC The present sequence represents a mutant endo-beta-1,4-xylanase. The
XX CC specification also describes an endo-beta-1,4-xylanase inhibitor, which
XX CC is obtained from wheat flour. The specification also describes a mutant
XX CC xylanase protein. The xylanase is useful for preparing a foodstuff.
XX CC preferably a bakery product or a substance (e.g. a dough) for making the
XX CC bakery product. Wild type xylanase or mutant xylanase is useful for
XX CC preparing a dough that is less sticky than a dough comprising a fungal
XX CC xylanase. The xylanase inhibitor is useful for screening high degree
XX CC resistance xylanases for dough preparation. The xylanase is also useful
XX CC for preparing a non-sticky dough. A combination of xylanase and the
XX CC inhibitor is useful for calibrating and/or determining the quantity of
XX CC inhibitor in a wheat flour sample
XX XX
SQ Sequence 213 AA;
Query Match 98.1%; Score 1149; DB 3; Length 213;
Best Local Similarity 97.7%; Pred. No. 1.3e-89;
Matches 208; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MFKFKNFLVGLSAAALMSISLFSATASAASTDYQNNWTDGGGIYNAVNGSGGNTSVNWSN 60
Db 1 MFKFKNFLVGLSAAALMSISLFSATASAASTDYQNNWTDGGGTNAVNGSGGNTSVNWSN 60
Qy 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLLTYGWTSPLEIYYVVDWSGTYRPTG 120
Db 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLLTYGWTSPLEIYYVVDWSGTYRPTG 120
Qy 121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRFTFTQYWSVRSKRPTGSNATITFSNHVNA 180
Db 121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRFTFTQYWSVRSKRPTGSNATITFSNHVNA 180
Qy 181 WKSHGMNLGSNWAYQVWMATEGYQSSGSSNTVTW 213
Db 181 WKSHGMNLGSNWAYQVWMATEGYKSSGSSNTVTW 213
RESULT 15
AAR47200
ID AAR47200 standard; protein; 213 AA.
XX XX
XX AC AAR47200;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 10-AUG-1994 (first entry)
XX XX
XX DE Modified xylanase of Bacillus subtilus.
XX XX

```

KW Xylanase; Bacillus subtilis; baking; bread; yeast; food; foodstuffs;  
XX bread; pastry.

OS Bacillus subtilis.

XX Key Location/Qualifiers

XX Peptide 1..28 /label= Signal peptide.

FT Misc-difference 7 /note= "Wild type amino acid substituted for Lys."

FT Misc-difference 13 /note= "Wild type amino acid substituted for Thr."

FT Misc-difference 16 /note= "Wild type amino acid substituted for Phe."

FT Misc-difference 21 /note= "Wild type amino acid substituted for Met."

FT Peptide 29..185 /label= Mature protein.

FT Misc-difference 30 /note= "Wild type amino acid substituted for Gly."

FT Misc-difference 43 /note= "Wild type amino acid substituted for Thr."

FT Misc-difference 150 /note= "Wild type amino acid substituted for Asn."

FT Misc-difference 171 /note= "Wild type amino acid substituted for Ala."

FT Misc-difference 197 /note= "Wild type amino acid substituted for Leu."

FT Misc-difference 203 /note= "Wild type amino acid substituted for Lys."

XX DE4226528-Al.

PN 17-FEB-1994.

XX 11-AUG-1992; 92DE-04226528.

XX 11-AUG-1992; 92DE-04226528.

XX (ROHG ) ROEHM GMBH.

XX Gottschalk M, Sproessler B, Schuster E;

XX WPI; 1994-050809/08.

DR N-PSDB; AAQ56052.

XX New xylanase obtd. from Bacillus subtilis - useful in baking agents for

XX increased vol. of baking prods.

XX Claim 4; Page 10; lipp; German.

XX The modified xylanase is used as a baking agent, preferably for yeast

CC pastry and white bread. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 213 AA;

SQ Query Match 96.5%; Score 1130; DB 2; Length 213;

Best Local Similarity 95.3%; Pred. No. 5.6e-88;

Matches 203; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MFKFKNPLVGLSALMSISLFSATASAASTDYQWQNTDGGIYVAVNGSGGNYSVNWSN 60

Db 1 MFKFKKFLVGLTAFAFMSISMFSAATAGTDYQWQNTDGGITVAVNGSGGNYSVNWSN 60

Qy 61 TGNFVVGKWTGTPFRITNYNAGVWAPNGYLTLYGWTSPLEIYVVDVSWGTYRPTG 120

Db 61 TGNFVVGKWTGTPFRITNYNAGVWAPNGYLTLYGWTSPLEIYVVDVSWGTYRPTG 120

Qy 121 TYKGTVKSDGGTYDIYITTRYNAPSIDGDRITFTQYWSVRSKRPSTGNAITTFSNHVNA 180

Db 121 TYKGTVKSDGGTYDIYITTRYNAPSIDGDRITFTQYWSVRSKRPSTGNAITTFSNHVNA 180

Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNTVW 213

4\*

Db 181 WKSHGMNLGSNWAYQVWATEGYKSSGSSNTVW 213

Search completed: February 3, 2006, 09:15:43  
Job time : 94 secs

**This Page Blank (uspto)**



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 3, 2006, 09:18:08 ; Search time 23 Seconds  
(without alignment)  
891.051 Million cell updates/sec

Title: US-10-626-583-5

Perfect score: 1171

Sequence: 1 MFPEKQFLVGLSLAALMSIS.....YQVMATEGYQSSGSSNTVTW 213

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1171	100.0	213	1 I40569	endo-1,4-beta-xyla
2	1168	99.7	213	1 S01734	endo-1,4-beta-xyla
3	1165	99.5	213	1 S48126	endo-1,4-beta-xyla
4	864.5	73.8	210	2 C83762	endo-1,4-beta-xyla
5	651.5	55.6	241	2 T37005	endo-1,4-beta-xyla
6	637	54.4	240	1 S05091	endo-1,4-beta-xyla
7	621	53.0	240	1 S47512	endo-1,4-beta-xyla
8	609.5	52.0	644	1 I40712	endo-1,4-beta-xyla
9	600	51.2	225	1 S57477	endo-1,4-beta-xyla
10	594	50.7	333	1 J05090	endo-1,4-beta-xyla
11	594	50.7	335	2 T50601	endo-1,4-beta-xyla
12	578	49.4	232	2 J07577	endo-1,4-beta-xyla
13	557	47.1	221	1 S57469	endo-1,4-beta-xyla
14	552	47.1	227	2 S43919	endo-1,4-beta-xyla
15	540	46.1	219	2 S71472	endo-1,4-beta-xyla
16	530	45.3	197	1 A44597	endo-1,4-beta-xyla
17	525	44.8	221	2 J07307	endo-1,4-beta-xyla
18	523	44.7	190	1 A44595	endo-1,4-beta-xyla
19	515.5	44.0	241	2 S71473	endo-1,4-beta-xyla
20	513	43.8	190	1 A44593	endo-1,4-beta-xyla
21	506	43.2	190	1 A44594	endo-1,4-beta-xyla
22	505	43.1	223	2 S39883	endo-1,4-beta-xyla
23	503	43.0	222	2 S39154	endo-1,4-beta-xyla
24	480.5	41.0	354	1 S51779	endo-1,4-beta-xyla
25	469	39.4	661	1 S51779	endo-1,4-beta-xyla
26	461.5	39.4	228	1 W953XP	endo-1,4-beta-xyla
27	436	37.2	656	1 S59631	endo-1,4-beta-xyla
28	420	35.9	261	1 S12745	endo-1,4-beta-xyla
29	409	34.9	511	1 JQ1935	endo-1,4-beta-xyla

#### RESULT 1

I40569

endo-1,4-beta-xylanase (EC 3.2.1.8) A precursor - Bacillus subtilis

N:Alternate names: xylanase A

C:Species: Bacillus subtilis

C>Date: 12-Aug-1996 #sequence\_revision 02-Jul-1998 #text change 09-Jul-2004

C:Accession: I40569; S39157; S39158; A53635; F69735; S51711

R:Wolf, M.; Geczi, A.; Simon, O.; Borriass, R.

Microbiology 141, 281-290, 1995

A>Title: Genes encoding xylan and beta-glucan hydrolysing enzymes in Bacillus subtilis:

A:Reference number: I40370; MUID:95219081; PMID:7704256

A:Accession: I40569

A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMF

A:Molecule type: DNA

A:Residues: 1-22,'P' 24-213 <WOL>

A:Cross-references: UNIPROT:P18429; UNIPARC:UPI00000863D0; EMBL:Z34519; NID:G2995396; P1

A:Experimental source: strain 168

R:Paice, M.G.; Bourbonnais, R.; Desrochers, M.; Jurasek, L.; Yaguchi, M.

Arch. Microbiol. 144, 201-206, 1986

A>Title: A xylanase gene from Bacillus subtilis: nucleotide sequence and comparison with

A:Reference number: S39157

A:Accession: S39157

A:Molecule type: DNA

A:Residues: 1-213 <PA11>

A:Cross-references: UNIPARC:UPI00000336C9; EMBL:M36648; NID:G143842; PIDN:AAA22897.1; J

A:Experimental source: strain PAP115

A:Accession: S39158

A:Molecule type: protein

A:Residues: 29-58;60-73;75-76 <PA12>

A:Cross-references: UNIPARC:UPI000015759E; UNIPARC:UPI0000172962; UNIPARC:UPI0000172963

A:Experimental source: strain PAP115

R:Miao, S.; Ziser, L.; Aebersold, R.; Withers, S.G.

Biochemistry 33, 7027-7032, 1994

A>Title: Identification of glutamic acid 78 as the active site nucleophile in Bacillus

A:Reference number: A53635; MUID:94271752; PMID:7911679

A:Accession: A53635

A:Status: preliminary

A:Molecule type: protein

A:Residues: 97-107 <MIA>

A:Cross-references: UNIPARC:UPI0000172964

R:Kunst, F.; Ogatawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter

C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho

A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallier

lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F.

Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Ladinois, A.; Lardinois,

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel

Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,

A:Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seror,

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipar, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.  
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Banchin, A. Bacillus subtilis.  
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A:Reference number: A69580; MUID:98044033; PMID:9384377  
A:Accession: F69735  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-213 <XUN>  
A:Cross-references: UNIPARC:UPI00000336C9; GB:Z99114; GB:AL009126; NID:g26342230; PIDN:CA  
A:Experimental source: strain 168  
C:Genetics:  
A:Gene: xynA  
A:Map position: 175 degrees  
C:Function:  
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans  
A:Pathway: xylan degradation  
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology  
C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation  
F:1-28/Domain: signal sequence #status predicted <SIG>  
F:29-213/Product: endo-1,4-beta-xylanase A #status experimental <MAT>  
F:31-213/Domain: endo-1,4-beta-xylanase homology <XYL>  
F:106/Active site: Glu #status predicted  
F:200/Active site: Glu #status predicted

Query Match 100.0%; Score 1171; DB 1; Length 213;  
Best Local Similarity 100.0%; Pred. No. 2.4e-80;  
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKFKNPLVGLSALMSISLFSATASAASTDYQWNTDGGGINVAVNGSGGNSVNWNS 60  
Db 1 MFKFKNPLVGLSALMSISLFSATASAASTDYQWNTDGGGINVAVNGSGGNSVNWNS 60

Qy 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDWSWGYRPTG 120  
Db 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDWSWGYRPTG 120

Qy 121 TYKGTVKSDDGTDIYITTRYNAPSIDGDRITFTQYWSVRSKRPTGSNATITFSNHVNA 180  
Db 121 TYKGTVKSDDGTDIYITTRYNAPSIDGDRITFTQYWSVRSKRPTGSNATITFSNHVNA 180

Qy 181 WKSHGMNLGSNWAYQVMATGEGYQSSGSSNVTVW 213  
Db 181 WKSHGMNLGSNWAYQVMATGEGYQSSGSSNVTVW 213

RESULT 2  
S01734  
endo-1,4-beta-xylanase (EC 3.2.1.8) A precursor [validated] - Bacillus circulans  
N:Alternate names: xylanase A  
C:Species: Bacillus circulans  
C:Date: 07-Jun-1990 #sequence\_revision 22-Nov-1996 #text\_change 09-Jul-2004  
C:Accession: S01734  
R:Yang, R.C.A.; MacKenzie, C.R.; Narang, S.A.  
Nucleic Acids Res. 16, 7187, 1988  
A:Title: Nucleotide sequence of a Bacillus circulans xylanase gene.  
A:Reference number: S01734; MUID:86303346; PMID:3405767  
A:Accession: S01734  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-213 <YAN>  
A:Cross-references: UNIPROT:P09850; UNIPARC:UPI0000034D1C; EMBL:X07723; NID:g39462; PIDN  
A>Note: part of this sequence, including the amino end of the mature protein, was confir  
R:Wakarchuk, W.W.; Campbell, R.L.; Sung, W.L.; Davoodi, J.; Yaguchi, M.  
Protein Sci. 3, 467-475, 1994  
A:Title: Mutational and crystallographic analyses of the active site residues of the Bac  
A:Reference number: A53181; MUID:94290322; PMID:8019418  
A:Contents: annotation; X-ray crystallography, 1.49 angstroms, residues 29-213  
R:Campbell, R.L.  
submitted to the Brookhaven Protein Data Bank, June 1994  
A:Reference number: A52866; PDB:1XNB  
A:Contents: annotation; X-ray crystallography, 1.49 angstroms, residues 29-213  
C:Genetics:  
A:Gene: xlnA

C:Function:  
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans  
A:Pathway: xylan degradation  
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology  
C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation  
F:1-28/Domain: signal sequence #status predicted <SIG>  
F:29-213/Product: endo-1,4-beta-xylanase A #status experimental <MAT>  
F:31-213/Domain: endo-1,4-beta-xylanase homology <XYL>  
F:97,108,140/Binding site: substrate (Tyr, Tyr, Arg) #status experimental  
F:106,200/Active site: Glu #status experimental

Query Match 99.7%; Score 1168; DB 1; Length 213;  
Best Local Similarity 99.5%; Pred. No. 3.9e-80;  
Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKFKNPLVGLSALMSISLFSATASAASTDYQWNTDGGGINVAVNGSGGNSVNWNS 60  
Db 1 MFKFKNPLVGLSALMSISLFSATASAASTDYQWNTDGGGINVAVNGSGGNSVNWNS 60

Qy 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDWSWGYRPTG 120  
Db 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDWSWGYRPTG 120

Qy 121 TYKGTVKSDDGTDIYITTRYNAPSIDGDRITFTQYWSVRSKRPTGSNATITFSNHVNA 180  
Db 121 TYKGTVKSDDGTDIYITTRYNAPSIDGDRITFTQYWSVRSKRPTGSNATITFSNHVNA 180

Qy 181 WKSHGMNLGSNWAYQVMATGEGYQSSGSSNVTVW 213  
Db 181 WKSHGMNLGSNWAYQVMATGEGYQSSGSSNVTVW 213

RESULT 3  
S48126  
endo-1,4-beta-xylanase (EC 3.2.1.8) S precursor - Bacillus sp. (strain YA-14)  
N:Alternate names: xylanase S  
C:Species: Bacillus sp.  
A:Variety: strain YA-14  
C:Date: 14-Jul-1995 #sequence\_revision 22-Nov-1996 #text\_change 09-Jul-2004  
C:Accession: S48126  
R:Ju-Hyun, Y.; Park, Y.S.; Yum, D.Y.; Kim, J.M.; Kong, I.S.; Bai, D.H.  
J. Microbiol. Biotechnol. 3, 139-145, 1993  
A:Title: Nucleotide sequence and analysis of a xylanase gene (xyns) from alkali-tolerant  
A:Reference number: S48126  
A:Accession: S48126  
A:Molecule type: DNA  
A:Residues: 1-213 <YUH>  
A:Cross-references: UNIPROT:Q59256; UNIPARC:UPI0000060D47; EMBL:X59058; NID:g458800; PII  
A:Experimental source: strain YA-14  
C:Genetics:  
A:Gene: xynS  
C:Function:  
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans  
A:Pathway: xylan degradation  
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology  
C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation  
F:1-28/Domain: signal sequence #status predicted <SIG>  
F:29-213/Product: endo-1,4-beta-xylanase S #status predicted <MAT>  
F:31-213/Domain: endo-1,4-beta-xylanase homology <XYL>  
F:106,200/Active site: Glu #status predicted

Query Match 99.5%; Score 1165; DB 1; Length 213;  
Best Local Similarity 99.1%; Pred. No. 6.6e-80;  
Matches 211; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKFKNPLVGLSALMSISLFSATASAASTDYQWNTDGGGINVAVNGSGGNSVNWNS 60  
Db 1 MFKFKNPLVGLSALMSISLFSATASAASTDYQWNTDGGGINVAVNGSGGNSVNWNS 60

Qy 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDWSWGYRPTG 120  
Db 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDWSWGYRPTG 120

```
QY 121 TYKGVKSDGGTYDYITTRYNAPSIDGRTTFTQWVSQRKPTGSGNATITFSNHVNA 180
DB 121 TYKGVKSDGGTYDYITTRYNAPSIDGRTTFTQWVSQRKPTGSGNATITFSNHVNA 180

QY 181 WKSHGMNLGNNWAYQVMATEGYQSSGSSNVTW 213
DB 181 WKSHGMNLGNNWAYQVMATEGYQSSGSSNVTW 213

RESULT 4
C3762
endo-1,4-beta-xylanhydrolase BH0899 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: C83762
R:Ikakami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: AB83650; MUID:20512582; PMID:11059132
A:Accession: C83762
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-210 <STO>
A:CROSS-references: UNIPROT:Q9KEP3; UNIPARC:UPI00000DCBD1; GB:AP001510; GB:BA000004; NID
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH0899
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology

Query Match 73.8%; Score 864.5; DB 2; Length 210;
Best Local Similarity 74.2%; Pred. No. 1.6e-57;
Matches 158; Conservative 19; Mismatches 33; Indels 3; Gaps 2;

QY 1 MPKFKNFLVLGLSALMSISLFSATASAASTDYQNWTDGGGIVNAVNGSGNYVNSN 60
DB 1 MPKFKVTGLTVVIAATISFCLSAVPASA--NTYQYWDGGGTGVTNATNGPGGNYSVTRD 58

QY 61 TGNFVVGKWTGSPFRINYNAGVWAPNGNGLYLKGWTRSPLEYIVVDSWGYRPTG 120
DB 59 TGNFVVGKWEIGSPNRIHYNAGVWEPGNGLYLKGWTRNQLLEYIVVDNWGYRPTG 118

QY 121 TYKGVKSDGGTYDYITTRYNAPSIDGRTTFTQWVSQRKPTGSGNATITFSNHVNA 180
DB 119 THRGFVSDGGTYDYITTRYNAPSIDGTQ-TFQQFWSVRSQRKPTGNNVSIITFSNHVNA 177

QY 181 WKSHGMNLGNNWAYQVMATEGYQSSGSSNVTW 213
DB 178 WRNAGMNLGSSWSYQVLATEGYQSSGSSNVTW 210

RESULT 5
T37005
endo-1,4-beta-xylanase - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T37005
R:Oliveir, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1999
A:Reference number: Z21618
A:Accession: T37005
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-241 <OLI>
A:CROSS-references: UNIPROT:Q9RI72; UNIPARC:UPI00000DB349; EMBL:AL109949; PIDN:CAB52919.
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: xinc; SCODB:SCJ11.34c
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology

Query Match 55.6%; Score 651.5; DB 2; Length 241;
Best Local Similarity 58.4%; Pred. No. 1.3e-41;
Matches 129; Conservative 25; Mismatches 50; Indels 17; Gaps 6;
```

```
QY 5 KKNFLVG---LSAALMSISLFSATASAAST-----DYQNWTDGGGIVNAVNGSG 51
DB 23 RRGFLGGAGTALATASGLLLPGTAHAATITTTQGTGDMGYSPFTDGGGVSMTLNGG 82

QY 52 GNYSVNSNTGNFVVGKWTGSPFRINYNAGVWAPNGNGLYLKGWTRSPLEYIVVVD 111
DB 83 GSYSQTQWTCNCGNFVAGKMGSTGGR-RTVRYN-GYFNPGNGYGCGLYGTWISNPLVEYIVD 140

QY 112 SWGTYRPTGTYKGVKSDGGTYDYITTRYNAPSIDGRTTFTQWVSQRKPTGSGNAT 171
DB 141 NMGYSRPTGTYKGVKSDGGTYDYITTRYNAPSVEGK-TFQQYWSVRQSKVTSGS-GT 198

QY 172 ITFSNHVNAWKSHGMNLGNNWAYQVMATEGYQSSGSSNVTW 212
DB 199 ITTGNHFDARAGNMNQFRYIMATEGYQSSGSSNITV 239

RESULT 6
J50591
endo-1,4-beta-xylanase (EC 3.2.1.8) C precursor - Streptomyces lividans
N:Alternate names: xylanase C
C:Species: Streptomyces lividans
C:Date: 14-Jul-1994 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C:Accession: J50591; PS0240
R:Shareck, F.; Roy, C.; Yaguchi, M.; Morosoli, R.; Kluepfel, D.
Gene 107, 75-82, 1991
A:Title: Sequences of three genes specifying xylanases in Streptomyces lividans.
A:Reference number: J50589; MUID:92077439; PMID:1743521
A:Accession: J50591
A:Molecule type: DNA
A:Residues: 1-240 <SHA>
A:CROSS-references: UNIPROT:P26220; UNIPARC:UPI0000034D31; GB:M64553; NID:g153530; PIDN
A:Accession: PS0240
A:Molecule type: protein
A:Residues: 50-80 <SH2>
A:CROSS-references: UNIPARC:UPI00000172965
C:Genetics:
A:Gene: xinc
C:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F:1-49/Domain: signal sequence #status predicted <SIG>
F:50-240/Product: endo-1,4-beta-xylanase C #status experimental <MAT>
F:62-239/Domain: endo-1,4-beta-xylanase homology <XYL>
F:134,226/Active site: Glu #status predicted

Query Match 54.4%; Score 637; DB 1; Length 240;
Best Local Similarity 57.5%; Pred. No. 1.6e-40;
Matches 127; Conservative 24; Mismatches 52; Indels 18; Gaps 6;

QY 5 KKNFLVG---LSAALMSISLFSATASAAST-----DYQNWTDGGGIVNAVNGSG 51
DB 23 RRGFLGGAGTALATASGLLLPGTAHAATITTTQGTGDMGYSPFTDGGGVSMTLNGG 82

QY 52 GNYSVNSNTGNFVVGKWTGSPFRINYNAGVWAPNGNGLYLKGWTRSPLEYIVVVD 111
DB 83 GSYSQTQWTCNCGNFVAGKMGSTGD--GNVRYN-GYFNPGNGYGCGLYGTWISNPLVEYIVD 139

QY 112 SWGTYRPTGTYKGVKSDGGTYDYITTRYNAPSIDGRTTFTQWVSQRKPTGSGNAT 171
DB 140 NMGYSRPTGTYKGVKSDGGTYDYITTRYNAPSVEGK-TFQQYWSVRQSKVTSGS-GT 197

QY 172 ITFSNHVNAWKSHGMNLGNNWAYQVMATEGYQSSGSSNVTW 212
DB 198 ITTGNHFDARAGNMNQFRYIMATEGYQSSGSSNITV 238

RESULT 7
S47512
endo-1,4-beta-xylanase (EC 3.2.1.8) precursor - Streptomyces sp.
N:Alternate names: xylanase
```

```

F;20-225/Product: endo-1,4-beta-xylanase 1 #status predicted <MAT>
F;48-235/Domain: endo-1,4-beta-xylanase homology <XYL>
F;121,212/Active site: Glu #status predicted

Query Match          51.2%;   Score 600;   DB 1;   Length 225;
Best Local Similarity 56.88;   Pred. No. 8,4e-38;
Matches 121; Conservative 29; Mismatches 41; Indels 22; Gaps

Qy      9  LVGLSALMISLFSATASAASTDYQN-----WTDGGGIVNAVNGSGGNYSVNWSNTG 62
Db      27  LAAREASLLERSPTSSGT-----NSNGYYYSFWDGGDVTYTNCGAGGSYTVQWSNVG 79

Qy     63  NFVVGKWTGSPFRTINYNAGWAPNGNGYLTLGYWTRSPLEIYYVVDWSGTYRP--TG 120
Db     80  NFVGGKWNPGST-RTINY--GGSFNPSPGNGYLAVYGWTONPLEIYYIVESYGTVPNGSGG 137

Qy    121  TYGKTGKSDGGTVDIYITTTTINAPSIDGRTITTFQWVSQRKPTGSGNATITFSNHVNA 180
Db    138  QHRGTVYSDGATYDIYATRYNAPSIEG-TATPEQFWSVRQSKRTGG---TVTTTANHFA 193

Qy    181  WKSHGMNLGNWAYQVMATGYOSSGSSNVTVM 213
Db    194  WAALGMRLGTH-NYQIVATEGYOSSGASITVY 225

RESULT 10
JS0590
endo-1,4-beta-xylanase (EC 3.2.1.8) B precursor - Streptomyces lividans
N;Alternate names: xylanase B
C;Species: Streptomyces lividans

```

C>Date: 10-Mar-1994 #sequence\_revision 22-Nov-1996 #text\_change 26-Feb-1999  
C:Accession: JS0590; PS0239  
R:Shareck, F.; Roy, C.; Yaguchi, M.; Morosoli, R.; Kluepfel, D.  
Gene 107, 77-82, 1991  
A:Title: Sequences of three genes specifying xylanases in Streptomyces lividans.  
A:Reference number: JS0589; MUID:92077439; PMID:1743521  
A:Accession: JS0590  
A:Molecule type: DNA  
A:Residues: 1-333 <SHA>  
A:CROSS-references: UNIPARC:UPI000017296A; GB:M64552  
A:Accession: PS0239  
A:Molecule type: protein  
A:Residues: 41-71 <SH2>  
A:CROSS-references: UNIPARC:UPI000017296B  
C:Genetics:  
A:Gene: xlnB  
C:Function:  
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans  
A:Pathway: xylan degradation  
C:Superfamily: Clostridium endo-1,4-beta-xylanase B; endo-1,4-beta-xylanase homology  
C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation  
F:1-40/Domain: signal sequence #status predicted <SIG>  
F:41-333/Product: endo-1,4-beta-xylanase B #status experimental <MAT>  
F:54-230/Domain: endo-1,4-beta-xylanase homology <XYL>  
F:127,217/Active site: Glu #status predicted

Query Match 50.7%; Score 594; DB 1; Length 333;  
Best Local Similarity 62.2%; Pred. No. 3.6e-37;  
Matches 112; Conservative 19; Mismatches 43; Indels 6; Gaps 4;

QY 33 YWQNTDGGGIVNAVNGSGGNYVNMSTGNFVVGKGTGSPPTINYNAGWAPNGNG 92  
DB 56 YISFMTDSQGTVMNMGSGGQYSTWRNTGNFVAGKWANGR-RTVQY-SGSFNPSSNA 113  
QY 93 YLTLYGWTSPLEIYYVVDVSWGTGYRPTGYKGTVKSDGTYDIYTTTTRYNAPSIDGDRTT 152  
DB 114 YLYLGTWSTNPLVEIYVDNMGTYRPTGEYKGTVTSDGTYDIYKTRVNKPSVETR-T 172  
QY 153 FTQYMSVRSKRPTGSNATITFSNHVNAWKSHGMNLGNWAYQVNMATGYQSSGSSNVTV 212  
DB 173 FDQYMSVRQAKRTGG---TITGNHFDARAGMPLGNFYSYMIATGEGYQSSGTSINV 229

RESULT 11  
T50601  
endo-1,4-beta-xylanase (EC 3.2.1.8) B, secreted [imported] - Streptomyces coelicolor  
N:Alternate names: xylanase B  
C:Species: Streptomyces coelicolor  
C>Date: 21-Jul-2000 #sequence\_revision 21-Jul-2000 #text\_change 09-Jul-2004  
C:Accession: T50601  
R:Redenbach, M.; Kieser, H.M.; Denapaite, D.; Eichner, A.; Cullum, J.; Kinashi, H.; Hopw Mol. Microbiol. 21, 77-96, 1996  
A:Title: A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb S  
A:Reference number: Z20556; MUID:97000351; PMID:8843436  
A:Accession: T50601  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-335 <RED>  
A:CROSS-references: UNIPROT:Q9RKN6; UNIPARC:UPI00000DC56E; EMBL:AL1133220; PIDN:CAB61738  
A:Experimental source: strain A3(2)  
C:Genetics:  
A:Gene: xlnB  
C:Superfamily: Clostridium endo-1,4-beta-xylanase B; endo-1,4-beta-xylanase homology  
C:Keywords: glycosidase; hydrolase

Query Match 50.7%; Score 594; DB 2; Length 335;  
Best Local Similarity 62.2%; Pred. No. 3.6e-37;  
Matches 112; Conservative 19; Mismatches 43; Indels 6; Gaps 4;

QY 33 YWQNTDGGGIVNAVNGSGGNYVNMSTGNFVVGKGTGSPPTINYNAGWAPNGNG 92  
DB 57 YISFMTDSQGTVMNMGSGGQYSTWRNTGNFVAGKWANGR-RTVQY-SGSFNPSSNA 114

QY 93 YLTLYGWTSPLEIYYVVDVSWGTGYRPTGYKGTVKSDGTYDIYTTTTRYNAPSIDGDRTT 152  
DB 115 YLYLGTWSTNPLVEIYVDNMGTYRPTGEYKGTVTSDGTYDIYKTRVNKPSVETR-T 173  
QY 153 FTQYMSVRSKRPTGSNATITFSNHVNAWKSHGMNLGNWAYQVNMATGYQSSGSSNVTV 212  
DB 174 FDQYMSVRQAKRTGG---TITGNHFDARAGMPLGNFYSYMIATGEGYQSSGTSINV 230

RESULT 12  
JC7577  
endo-1,4-beta-xylanase (EC 3.2.1.8) G2 - Aspergillus oryzae  
N:Alternate names: endo-1,3-beta-xylanase G2; xylanase G2  
C:Species: Aspergillus oryzae  
C>Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 09-Jul-2004  
C:Accession: JC7577; PC7120  
R:Kimura, T.; Suzuki, H.; Furuhashi, H.; Aburatani, T.; Morimoto, K.; Karita, S.; Sakka, Biosci. Biotechnol. Biochem. 64, 2734-2738, 2000  
A:Title: Molecular cloning, overexpression, and purification of a major xylanase from A:  
A:Reference number: JC7577; MUID: 21077500; PMID:111210150  
A:Accession: JC7577  
A:Molecule type: DNA  
A:Residues: 1-232 <KIN>  
A:CROSS-references: UNIPROT:Q9HFA4; UNIPARC:UPI0000069976; DDBJ:AB044941  
A:Experimental source: strain KEN616  
A:Accession: PC7120  
A:Molecule type: protein  
A:Residues: 45-64 <K12>  
A:CROSS-references: UNIPARC:UPI0000175A84  
C:Comment: This enzyme has strong similarity to other fungal family 11 endoxylanases, d:  
C:Genetics:  
A:Gene: xynG2  
A:Introns: 100/2  
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology  
C:Keywords: glycosidase; hydrolase

Query Match 49.4%; Score 578; DB 2; Length 232;  
Best Local Similarity 52.1%; Pred. No. 3.8e-36;  
Matches 122; Conservative 31; Mismatches 47; Indels 34; Gaps 9;

QY 7 NFLVGLSAAALMSIS-----LFSATA-----SAASTD-----YWNQNTDGG 41  
DB 6 SILLACSAAGALATPIEPLADHPNEAFNETAFDLVGRSTPSTGYNNGYYSPWTDGG 65  
QY 42 GIVNAVNGSGGNYVNMSTGNFVVGKGTGSPPTINYNAGWAPNGNGHLYTGWTR 101  
DB 66 GDVITYTNGGSGSYVQNSNVGNFVGGKGNPQSS-RAITY-SGSFNPSSGNGYLAVYGTWT 123  
QY 102 SPLIYYVVDVSWGTGYRPTGYKGTVKSDGTYDIYTTTTRYNAPSIDGDRTTFTQYMSV 159  
DB 124 DPLIYYIVESYGTYNPGSGGTGKQVTSDDGTYNITSVRTNAPSIIIG-TATFTQFWSV 182  
QY 160 ROSKRPTGSNATITFSNHVNAWKSHGMNLGNWAYQVNMATGYQSSGSSNVTVM 213  
DB 183 RTSKRVGS---TVTGNHFNWAKYGLTLGTH-NYQIVATGEGYQSSGSAITVY 232

RESULT 13  
S57469  
endo-1,4-beta-xylanase (EC 3.2.1.8) 2 precursor - Emericella nidulans  
N:Alternate names: xylanase 2  
C:Species: Emericella nidulans, Aspergillus nidulans  
C>Date: 10-Oct-1995 #sequence\_revision 22-Nov-1996 #text\_change 09-Jul-2004  
C:Accession: S57469  
R:Perez-Gonzalez, J.A.  
submitted to the EMBL Data Library, June 1995  
A:Description: Expression in Saccharomyces cerevisiae of two xylanase encoding genes fr:  
A:Reference number: S57469  
A:Accession: S57469  
A:Molecule type: DNA  
A:Residues: 1-221 <PER>  
A:CROSS-references: UNIPROT:P55333; UNIPARC:UPI0000139075; EMBL:Z49893; NID:g870834; PII:  
C:Genetics:

Db 118 PLVEYYIESYGTYNPGSQAQYKGTFFYTDGDDQYDIFVSTRYNQPSIDGTR-TFQQYWSIR 176

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 3, 2006, 09:15:58 ; Search time 108 Seconds  
(without alignments)  
1391.459 Million cell updates/sec

Title: US-10-626-583-5

Perfect score: 1171

Sequence: 1 MFPEKKFLVGLSALMSIS.....YQVMATEGYQSSGSNTVTW 213

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_crembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1171	100.0	213	1 Xyna_BACSU	P18429 bacillus su
2	1168	99.7	213	1 Xyna_BACCI	P09850 bacillus ci
3	1166	99.6	213	2 Q59254 BACSU	Q59254 bacillus su
4	1165	99.5	213	2 Q59256 9BACI	Q59256 bacillus sp
5	1150	98.2	213	2 Q8RMN9 BACSU	Q8RMN9 bacillus su
6	1144	97.7	213	2 Q8RMN8 BACCI	Q8RMN8 bacillus ci
7	1127	96.2	213	2 Q82B36 BACSP	Q82B36 bacillus sp
8	1104	94.3	213	2 Q84F19 9BACI	Q84F19 bacillus sp
9	1096	93.6	213	2 Q8VVC3 9BACI	Q8VVC3 bacillus sp
10	945.5	80.7	212	2 Q9F9B9 9BACL	Q9F9B9 paenibacill
11	935.5	79.9	214	2 Q6TLP3 9BACT	Q6TLP3 uncultured
12	930	79.4	210	1 Xyna_BACST	P45705 bacillus st
13	929	79.3	211	2 Q43993 AERPU	Q43993 aeromonas p
14	864.5	73.8	210	2 Q71S35 BACFI	Q71S35 bacillus fi
15	864.5	73.8	210	2 Q9KEF3 BACHD	Q9KEF3 bacillus ha
16	863.5	73.7	210	2 Q6U894 BACFI	Q6U894 bacillus fi
17	663.5	56.7	335	2 Q8R088 9MICO	Q8R088 xylanimicro
18	659	56.3	338	2 Q56285 THEFU	Q56285 thermomonos
19	659	56.3	338	2 Q8Z998 THEFU	Q8Z998 thermomonos
20	651.5	55.6	241	2 Q9R172 STRCO	Q9R172 streptomyce
21	646	55.2	329	2 Q9RMH9 STRVD	Q9RMH9 streptomyce
22	645.5	55.1	335	2 Q9RMW4 STRTM	Q9RMW4 streptomyce
23	639.5	54.6	335	2 Q76BV2 STRTL	Q76BV2 streptomyce
24	637	54.4	240	1 XINC_STRLI	P28220 streptomyce
25	636	53.8	344	2 Q8GMV7 9ACTO	Q8GMV7 nonomuraea
26	630	53.5	191	2 Q9EW89 STROI	Q9EW89 streptomyce
27	622	53.1	228	2 Q59962 9ACTO	Q59962 streptomyce
28	621.5	53.1	228	2 Q4WG11 ASPFU	Q4WG11 aspergillus
29	621	53.0	240	2 Q56013 9ACTO	Q56013 streptomyce
30	610.5	52.1	417	2 Q593B5 9ALTE	Q593B5 microbulbif
31	609.5	52.0	644	1 XYND_CELFI	P54865 cellulomona

RESULT 1  
Xyna\_BACSU  
ID Xyna\_BACSU

STANDARD; PRT; 213 AA.

ALIGNMENTS

32	609	52.0	346	2	Q8VUT4_9PSED	Q8VUT4 pseudomonas
33	600	51.2	225	1	Xyna_EMENI	P55332 emericella
34	600	51.2	225	1	Q5B767 EMENI	Q5B767 aspergillus
35	597	51.0	335	1	XYNB_STRLI	P26515 streptomyce
36	594	50.7	335	2	Q9RKN6 STRCO	Q9RKN6 streptomyce
37	587.5	50.2	220	2	Q7SDQ1 NEUCR	Q7sdq1 neurospora
38	585.5	50.0	230	2	Q8J1V5_9PEZI	Q8j1v5 chaetomium
39	583.5	49.8	225	2	Q8TG22 ASPNG	Q8tg22 aspergillus
40	583.5	49.8	225	2	Q6QA21_9EURO	Q6qa21 aspergillus
41	582	49.7	221	2	Q5AQH5 EMENI	Q5aqh5 aspergillus
42	581	49.6	225	1	XYN2 ASPNG	P55330 aspergillus
43	578	49.4	232	2	Q9HFA4 ASPOR	Q9hfa4 aspergillus
44	577	49.3	221	1	XYNB_EMENI	P55333 emericella
45	573.5	49.0	225	1	XYNB_ASPXA	P48824 aspergillus

AC P18429;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) (Xylanase A) (1,4-beta-D-xylan xylanohydrolase A).  
GN Name=xynA; OrderedLocusNames=BSU18840;  
OS Bacillus subtilis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1423;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Palce M.G., Bourbonnais R., Desrochers M., Jurasek L., Yaguchi M.;  
RT "A xylanase gene from Bacillus subtilis: nucleotide sequence and  
RT comparison with B. pumilus gene";  
RL Arch. Microbiol. 144:201-206(1986).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Lapidus A., Galleron N., Sorokin A., Ehrlich S.D.;  
RT "Sequence analysis of the Bacillus subtilis chromosome region between  
RT the terC and chrAB loci cloned in a yeast artificial chromosome";  
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=168;  
EX MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;  
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,  
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,  
RA Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,  
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,  
RA Chou S.-K., Codani J.-J., Connerton I.F., Cummings N.J., Daniel R.A.,  
RA Denizot F., Devine K.M., Duesterhoeft A., Ehrlich S.D., Emmerson P.T.,  
RA Entian K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,  
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,  
RA Ghim S.-Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,  
RA Guisepi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,  
RA Hilbert H., Holsappel S., Hosono S., Hulio M.-F., Itaya M.,  
RA Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,  
RA Klein C., Kobayashi Y., Koetter F., Koningsstein G., Krogh S.,  
RA Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,  
RA Lazarevic V., Lee S.-M., Levine A., Liu H., Masuda S., Maue C.,  
RA Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,  
RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,  
RA Park S.-H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,  
RA Prescott A.M., Prescan E., Pujic P., Purnelle B., Rapoport G.,  
RA Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,  
RA Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R.,  
RA Scoffone F., Sekiguchi J., Sekowska A., Seter S.J., Serror P.,  
RA Shin B.-S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,  
RA Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpsira P.,  
RA Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,

RA Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H.,  
 RA Weitzenecker T., Winters P., Wipat A., Yamamoto H., Yamane K.,  
 RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H.-F., Zumstein E.,  
 RA Yoshikawa H., Danchin A.;  
 RT "The complete genome sequence of the Gram-positive bacterium *Bacillus*  
 RT subtilis";  
 RL Nature 390:249-256(1997).  
 RN [4]  
 RN MUTAGENESIS.  
 RP Wakarchuk W., Methot N., Lanthier P., Sung W., Seligy V., Yaguchi M.,  
 RA To R., Campbell R., Rose D.;  
 RL (in) Vasser J., Belman G., Kusters-van Someren M.A., Voragen A.G.J.  
 RL (eds.);  
 RL Xylans and xylanases, pp.439-442, Elsevier, Amsterdam (1992).  
 RN [5]  
 RN ACTIVE SITE GLU-106.  
 RX MEDLINE=94271752; PubMed=7911679;  
 RA Miao S., Ziser L., Rebersold R., Withers S.G.;  
 RT "Identification of glutamic acid 78 as the active site nucleophile in  
 RT *Bacillus subtilis* xylanase using electrospray tandem mass  
 RT spectrometry.";  
 RL Biochemistry 33:7027-7032(1994).  
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic  
 CC linkages in xylans.  
 CC -!- PATHWAY: Xylan degradation.  
 CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 11 (cellulase G)  
 CC family.  
 CC  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC  
 DR EMBL; M36648; AAA22897.1; -; Genomic DNA.  
 DR EMBL; AF027868; AAB84458.1; -; Genomic DNA.  
 DR EMBL; Z99114; CAB13776.1; -; Genomic DNA.  
 DR PIR; I40569; I40569.  
 DR SDR; IAXK; X-ray; A/B=-.  
 DR SDR; PI8429; 27-213.  
 DR Subtilist; BG10808; xyna.  
 DR InterPro; IPR001137; Glyco\_hydro\_11.  
 DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
 DR PRINTS; PR00911; GLHYDRLASE11.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 KW 3D-structure; Complete proteome; Glycosidase; Hydrolase; Signal;  
 KW Xylan degradation.  
 FT SIGNAL 1 28  
 FT CHAIN 29 213  
 FT ACT\_SITE 106 106  
 FT MUTAGEN E->S: Drastically reduced activity.  
 FT MUTAGEN E->S: Drastically reduced activity.  
 SQ SEQUENCE 213 AA; 23345 MW; 20CBA35238CC0564 CRC64;  
  
 Query Match 100.0%; Score 1171; DB 1; Length 213;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-86;  
 Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 MPKPKNFVLGLSALMSISLFSATASASTDYQWNTDGGGINVAVNGSGNYSVNWNS 60  
 Db 1 MPKPKNFVLGLSALMSISLFSATASASTDYQWNTDGGGINVAVNGSGNYSVNWNS 60  
  
 QY 61 TGNFVVGKWTGSPFRINTNAGVWAPNGYLLYGTWTSPLLEYVVDWSGTYRPTG 120  
 Db 61 TGNFVVGKWTGSPFRINTNAGVWAPNGYLLYGTWTSPLLEYVVDWSGTYRPTG 120  
  
 QY 121 TYKGTVKSDGGTYDYITTYTRNAPSIDGDRTTFTQYWSVRQSKRPTGSNATIFSNHVA 180  
 Db 121 TYKGTVKSDGGTYDYITTYTRNAPSIDGDRTTFTQYWSVRQSKRPTGSNATIFSNHVA 180  
  
 QY 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVM 213

Db 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVM 213

# RESULT 2

XNA\_BACCI STANDARD; PRT; 213 AA.  
 AC P09850;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Endo-1,4-beta-xylanase precursor (EC 3.2.1.8) (Xylanase) (1,4-beta-D-  
 DE xylan xylanohydrolase).  
 GN Name=xlnA;  
 OS *Bacillus* circulans.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.  
 OX NCBI\_TaxID=1397;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=88303346; PubMed=3405767;  
 RA Yang R.C.A., Mackenzie C.R., Narang S.A.;  
 RT "Nucleotide sequence of a *Bacillus* circulans xylanase gene.";  
 RL Nucleic Acids Res. 16:7187-7187(1988).  
 RN [2]  
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS), AND MUTAGENESIS.  
 RX MEDLINE=94290322; PubMed=8019418;  
 RA Wakarchuk W.W., Campbell R.L., Sung W.L., Davoodi J., Yaguchi M.;  
 RT "Mutational and crystallographic analyses of the active site residues  
 RT of the *Bacillus* circulans xylanase.";  
 RL Protein Sci. 3:467-475(1994).  
 RN [3]  
 RP STRUCTURE BY NMR.  
 RX MEDLINE=96322313; PubMed=8756457; DOI=10.1021/bi9613234;  
 RA McIntosh L.P., Hand G., Johnson P.E., Joshi M.D., Koerner M.,  
 RA Plesniak L.A., Ziser L., Wakarchuk W.W., Withers S.G.;  
 RT "The pKa of the general acid/base carboxyl group of a glycosidase  
 RT cycles during catalysis: a 13C-NMR study of *Bacillus* circulans  
 RT xylanase.";  
 RL Biochemistry 35:9958-9966(1996).  
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic  
 CC linkages in xylans.  
 CC -!- PATHWAY: Xylan degradation.  
 CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 11 (cellulase G)  
 CC family.  
 CC  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC  
 DR EMBL; X07723; CAA30553.1; -; Genomic DNA.  
 DR PIR; S01734; S01734.  
 DR PDB; 1BCX; X-ray; @=29-213.  
 DR PDB; 1BVV; X-ray; @=29-213.  
 DR PDB; 1C5H; X-ray; A=29-213.  
 DR PDB; 1C5I; X-ray; A=29-213.  
 DR PDB; 1HV0; X-ray; A=29-213.  
 DR PDB; 1HV1; X-ray; A=29-213.  
 DR PDB; 1XNB; X-ray; @=29-213.  
 DR PDB; 1XNC; X-ray; @=29-213.  
 DR PDB; 2BVV; X-ray; A=29-213.  
 DR InterPro; IPR001137; Glyco\_hydro\_11.  
 DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
 DR PROSITE; PR00911; GLHYDRLASE11.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; 1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 KW 3D-structure; Glycosidase; Hydrolase; Signal; Xylan degradation.  
 FT SIGNAL 1 28  
 FT CHAIN 29 213  
 FT ACT\_SITE 106 106  
 FT ACT\_SITE 200 200  
 FT STRAND 33 38



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FT STRAND 43 48
FT TURN 51 52
FT STRAND 53 59
FT STRAND 63 70
FT TURN 75 76
FT STRAND 78 89
FT STRAND 92 101
FT TURN 102 104
FT STRAND 105 113
FT STRAND 121 128
FT TURN 129 130
FT STRAND 131 144
FT TURN 146 147
FT STRAND 150 160
FT STRAND 170 173
FT HELIX 174 183
FT TURN 184 185
FT STRAND 191 202
FT STRAND 205 213
SQ SEQUENCE 213 AA; 23359 MW; 4BA0A35238CC0135 CRC64;

Query Match 99.7%; Score 1168; DB 1; Length 213;
Best Local Similarity 99.5%; Pred. No. 4e-86;
Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFKFKNFLVGLSALMSISLFSATASASTDYQWQNTDGGGIVNAVNGSGGNYSVNWSN 60
DB 1 MFKFKNFLVGLSALMSISLFSATASASTDYQWQNTDGGGIVNAVNGSGGNYSVNWSN 60

QY 61 TGNFVVGKGTGSPFRITNINAGVWAPNGNGYLYGWTRSPLEYVVDVDSWGTYPRTG 120
DB 61 TGNFVVGKGTGSPFRITNINAGVWAPNGNGYLYGWTRSPLEYVVDVDSWGTYPRTG 120

QY 121 TYKGTVKSDGGTYDIYITTRYNAPSIDGDRITFTQYWSVRSKRPTGNSNATITFSNHVNA 180
DB 121 TYKGTVKSDGGTYDIYITTRYNAPSIDGDRITFTQYWSVRSKRPTGNSNATITFSNHVNA 180

QY 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
DB 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213

RESULT 3
Q59254 BACSU PRELIMINARY; PRT; 213 AA.
AC Q59254;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Xylanase (EC 3.2.1.8).
GN Name=xynA;
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=168 trpC2;
RX MEDLINE=92140374; PubMed=1310524;
RA Nierebach M., Kreuzaler F., Geerse R.H., Postma P.W., Hirsch H.J.;
RT "Cloning and nucleotide sequence of the Escherichia coli K-12 ppsA
gene, encoding PEP synthase.";
RL Mol. Gen. Genet. 231:332-336(1992).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=168 trpC2;
RX MEDLINE=95219081; PubMed=7704256;
RA Wolf M., Geczi A., Simon O., Borriass R.;
RT "Genes encoding xylan and beta-glucan hydrolysing enzymes in Bacillus
subtilis: characterization, mapping and construction of strains
deficient in lichenase, cellulase and xylanase.";
RL Microbiology 141:281-290(1995).
RN [3]
RP NUCLEOTIDE SEQUENCE.
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RC STRAIN=168 trpC2;
RA Borriass R., Wolf M.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z34519; CAA84276.1; -; Genomic_DNA.
DR HSSP; P09850; 1XNB.
DR SMR; Q59254; 27-213.
DR GO; GO:0031176; F:endo-1,4-beta-xylanase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0045493; P:xylan catabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Glycosidase; Hydrolase; Xylan degradation.
SQ SEQUENCE 213 AA; 23355 MW; 21D76D4F8CED4B7 CRC64;

Query Match 99.6%; Score 1166; DB 2; Length 213;
Best Local Similarity 99.5%; Pred. No. 5.8e-86;
Matches 212; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFKFKNFLVGLSALMSISLFSATASASTDYQWQNTDGGGIVNAVNGSGGNYSVNWSN 60
DB 1 MFKFKNFLVGLSALMSISLFSATASASTDYQWQNTDGGGIVNAVNGSGGNYSVNWSN 60

QY 61 TGNFVVGKGTGSPFRITNINAGVWAPNGNGYLYGWTRSPLEYVVDVDSWGTYPRTG 120
DB 61 TGNFVVGKGTGSPFRITNINAGVWAPNGNGYLYGWTRSPLEYVVDVDSWGTYPRTG 120

QY 121 TYKGTVKSDGGTYDIYITTRYNAPSIDGDRITFTQYWSVRSKRPTGNSNATITFSNHVNA 180
DB 121 TYKGTVKSDGGTYDIYITTRYNAPSIDGDRITFTQYWSVRSKRPTGNSNATITFSNHVNA 180

QY 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
DB 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213

RESULT 4
Q59256 9BACI PRELIMINARY; PRT; 213 AA.
AC Q59256;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Endo-1, 4-beta-xylanase precursor (EC 3.2.1.8).
GN Name=xynS;
OS Bacillus sp. VA-14.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=72411;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VA-14;
RA Yu J.H., Park Y.S., Yum D.Y., Kim J.M., Kong I.S., Bai D.H.;
RT "Nucleotide sequence and analysis of a xylanase gene (xynS) from
alkali-tolerant Bacillus sp. VA-14 and comparison with other
xylanases.";
RL J. Microbiol. Biotechnol. 3:139-145(1993).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VA-14;
RA Hyun Ju Y.;
RL Submitted (DEC-1990) to the EMBL/GenBank/DBJ databases.
DR EMBL; X59058; CAA41783.1; -; Genomic_DNA.
DR PIR; S48126; S48126.
DR HSSP; P09850; 1XNB.
DR SMR; Q59256; 27-213.
DR GO; GO:0031176; F:endo-1,4-beta-xylanase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0045493; P:xylan catabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
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DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Glycosidase; Hydrolase; Signal; Xylan degradation.
FT SIGNAL 1 28 Potential.
FT CHAIN 29 213 endo-1, 4-beta-xylanase.
SQ SEQUENCE 213 AA; 23341 MW; 2110D35768CC0034 CRC64;

Query Match 99.5%; Score 1165; DB 2; Length 213;
Best Local Similarity 99.1%; Pred. No. 7e-86;
Matches 211; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKEKKNFLVGLSAALMSISLFSATASATDYQWQNTDGGGIYVNAVNGSGNYSVNWNS 60
Db 1 MFKEKKNFLVGLSAALMSISLFSATASATDYQWQNTDGGGIYVNAVNGSGNYSVNWNS 60
Qy 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTG 120
Db 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTG 120
Qy 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVNA 180
Db 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVNA 180
Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTVM 213
Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTVM 213

RESULT 5
Q8RMN9_BACSU PRELIMINARY; PRT; 213 AA.
AC Q8RMN9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2003 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Endo-1,4-xylanase.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sun J., Gu S., Li W., Xiao H., Xiao J., Fu L.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF490979; AAM08359.1; -; Genomic_DNA.
DR HSSP; P09850; 1XNB.
DR SMR; Q8RMN9; 27-213.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0045493; P:xylan catabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR Xylan degradation.
KW Xylan degradation.
SQ SEQUENCE 213 AA; 23277 MW; 34DFAD4D9C2C0034 CRC64;

Query Match 98.2%; Score 1150; DB 2; Length 213;
Best Local Similarity 98.6%; Pred. No. 1.1e-84;
Matches 210; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MFKEKKNFLVGLSAALMSISLFSATASATDYQWQNTDGGGIYVNAVNGSGNYSVNWNS 60
Db 1 MFKEKKNFLVGLSAALMSISLFSATASATDYQWQNTDGGGIYVNAVNGSGNYSVNWNS 60
Qy 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTG 120
Db 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTG 120
Qy 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVNA 180
Db 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVNA 180
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Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTVM 213
Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTVM 213

RESULT 6
Q8RMN8_BACCI PRELIMINARY; PRT; 213 AA.
AC Q8RMN8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2003 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Endo-1,4-xylanase.
OS Bacillus circulans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1397;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sun J., Xu Z., Li W., Gu S., Zhao H., Xiao J., Chen Y.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF490980; AAM08360.1; -; Genomic_DNA.
DR HSSP; P09850; 1XNB.
DR SMR; Q8RMN8; 27-213.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0045493; P:xylan catabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR Xylan degradation.
KW Xylan degradation.
SQ SEQUENCE 213 AA; 23378 MW; E306B98D49E8CF4D CRC64;

Query Match 97.7%; Score 1144; DB 2; Length 213;
Best Local Similarity 97.4%; Pred. No. 3.4e-84;
Matches 208; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MFKEKKNFLVGLSAALMSISLFSATASATDYQWQNTDGGGIYVNAVNGSGNYSVNWNS 60
Db 1 MFKEKKNFLVGLSAALMSISLFSATASATDYQWQNTDGGGIYVNAVNGSGNYSVNWNS 60
Qy 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTG 120
Db 61 TGNFVVGKGTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTG 120
Qy 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVNA 180
Db 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGDRITFTQYWSVRQSKRPTGSNATITFSNHVNA 180
Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTVM 213
Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTVM 213

RESULT 7
Q9ZB36_BACSP PRELIMINARY; PRT; 213 AA.
AC Q9ZB36;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Endo-1,4-beta-xylanhydrolase.
GN Name=xynA;
OS Bacillus sp.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1409;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kim S.C., Jeong K.J., Kim M.S.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U51675; AAD10834.1; -; Genomic_DNA.
DR HSSP; P09850; 1XNB.
DR SMR; Q9ZB36; 27-213.
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DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004553; P:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
KW Hydrolase.
SQ SEQUENCE 213 AA; 23277 MW; 3A1DEE1139E3358B CRC64;

Query Match 96.2%; Score 1127; DB 2; Length 213;
Best Local Similarity 94.8%; Pred. No. 8e-83;
Matches 202; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 MFKFKNFVGLSLAALMSISLFSATASASTDYQWQNTDGGGVNAGVNGSGGNYSVNWSN 60
DB 1 MFKFKNFVGLSLAALMSISLFSATASASTDYQWQNTDGGGVNAGVNGSGGNYSVNWSN 60
QY 61 TGNFVVGKWTGSPFRITNINAGVWAPNGNGYLTLYGWTRSPLEIYYVVDGSGTYRPTG 120
DB 61 TGNFVVGKWTGSPFRITNINAGVWAPNGNGYLTLYGWTRSPLEIYYVVDGSGTYRPTG 120
QY 121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGRTTFTQYWSVRQSKRPTGSGNATITFSNHVNA 180
DB 121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGRTTFTQYWSVRQSKRPTGSGNATITFSNHVNA 180
QY 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
DB 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213

RESULT 8
Q84F19_9BACI PRELIMINARY; PRT; 213 AA.
AC Q84F19;
DT 01-JUN-2003 (TremBLrel. 24, Created)
DT 01-JUN-2003 (TremBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Endo-1,4-beta-xylanase A precursor.
GN Name=xynA;
OS Bacillus sp. BP-7.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=126733;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15057452; DOI=10.1007/s00284-003-4196-0;
RA Gallardo O., Diaz P., Pastor F.I.J.;
RT "Cloning and characterization of xylanase A from the strain Bacillus
sp. BP-7: comparison with alkaline pi-low molecular weight xylanases
of family 11.";
RL Curr. Microbiol. 48:276-279(2004).
DR EMBL; AJ536759; CAD60654.1; -; Genomic_DNA.
DR HSSP; P09850; 1XNB.
DR SMR; Q84F19; 27-213.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0045493; P:xylan catabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Signal; Xylan degradation.
FT SIGNAL 1 28 Potential.
FT CHAIN 29 213 endo-1,4-beta-xylanase A.
SQ SEQUENCE 213 AA; 23475 MW; F1E194D24A329516 CRC64;

Query Match 94.3%; Score 1104; DB 2; Length 213;
Best Local Similarity 93.0%; Pred. No. 5.7e-81;
Matches 198; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 MFKFKNFVGLSLAALMSISLFSATASASTDYQWQNTDGGGVNAGVNGSGGNYSVNWSN 60
DB 1 MFKFKNFVGLSLAALMSISLFSATASASTDYQWQNTDGGGVNAGVNGSGGNYSVNWSN 60
QY 61 TGNFVVGKWTGSPFRITNINAGVWAPNGNGYLTLYGWTRSPLEIYYVVDGSGTYRPTG 120
DB 61 TGNFVVGKWTGSPFRITNINAGVWAPNGNGYLTLYGWTRSPLEIYYVVDGSGTYRPTG 120
QY 121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGRTTFTQYWSVRQSKRPTGSGNATITFSNHVNA 180
DB 121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGRTTFTQYWSVRQSKRPTGSGNATITFSNHVNA 180
QY 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
DB 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213

RESULT 9
Q8VVC3_9BACI PRELIMINARY; PRT; 213 AA.
AC Q8VVC3;
DT 01-MAR-2002 (TremBLrel. 20, Created)
DT 01-MAR-2002 (TremBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Endo-xylanase.
GN Name=xylS;
OS Bacillus sp. NBL420.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=165829;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hong I.P., Lee S.Y., Choi S.G.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF441773; AAL32473.1; -; Genomic_DNA.
DR HSSP; P09850; 1XNB.
DR SMR; Q8VVC3; 27-213.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0045493; P:xylan catabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Xylan degradation.
SQ SEQUENCE 213 AA; 23341 MW; 4CC0DFF525E7551 CRC64;

Query Match 93.6%; Score 1096; DB 2; Length 213;
Best Local Similarity 92.5%; Pred. No. 2.5e-80;
Matches 197; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 MFKFKNFVGLSLAALMSISLFSATASASTDYQWQNTDGGGVNAGVNGSGGNYSVNWSN 60
DB 1 MFKFKNFVGLSLAALMSISLFSATASASTDYQWQNTDGGGVNAGVNGSGGNYSVNWSN 60
QY 61 TGNFVVGKWTGSPFRITNINAGVWAPNGNGYLTLYGWTRSPLEIYYVVDGSGTYRPTG 120
DB 61 TGNFVVGKWTGSPFRITNINAGVWAPNGNGYLTLYGWTRSPLEIYYVVDGSGTYRPTG 120
QY 121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGRTTFTQYWSVRQSKRPTGSGNATITFSNHVNA 180
DB 121 TYKGTVKSDGGTYDIYTTTRYNAPSIDGRTTFTQYWSVRQSKRPTGSGNATITFSNHVNA 180
QY 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
DB 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213

RESULT 10
Q9F9B9_9BACL PRELIMINARY; PRT; 212 AA.
AC Q9F9B9;
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
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DE Xylanase A.
OS Paenibacillus sp. KCTC8848P.
OC Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
OX NCBI_TaxID=109199;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=KCTC 8848P;
RA Lee H.J., Shin D.J., Cho N.C., Im S.Y., Lee H.B., Chun S.B., Bai S.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF195421; AAG33526.1; -; Genomic_DNA.
DR HSSP; P09850; 1XNB.
DR SMR; Q9P89; 25-212.
DR GO; GO:0004533; P:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0045493; P:xylan catabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; UNKNOWN_1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Xylan degradation.
SQ SEQUENCE 212 AA; 23258 MW; 1A1ABC825BED93D2 CRC64;

Query Match 80.7%; Score 945.5; DB 2; Length 212;
Best Local Similarity 79.3%; Pred. No. 3.2e-68;
Matches 169; Conservative 17; Mismatches 26; Indels 1; Gaps 1;

Qy 1 MFKFKNPLVGLSALMSISLFSATASAASTDYQWNTDGGGINVAVNGSGGYSVNMNSN 60
Db 1 MFKSSKLLTVVLAASMSFGFFASTSNA--TDYQWNTDGGGTNAVNGSGGYSVTWKN 59

Qy 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLYTGWTRSPLEIYVVDVDSWGTYRPTG 120
Db 60 SGNFVVGKWTGSPDRITINYNAGVWAPSGNGYLYGWTRNSLIYVVDVDSWGTYRPTG 119

Qy 121 TYKGTVKS DGTGYDIYTTTTRYNAPSIDGRTTFTQYWSVRQSKRPTGNSNATITFSNHVN 180
Db 120 TYKGTVTS DGTGYDIYTTTMRVDAPSIEGQKTTFTQYWSVRQTKRPTGKNTITFSNHVKA 179

Qy 181 WKSHGMNLSNWAYOVNATEGYQSSGSSNVTW 213
Db 180 WARQGMHLGNWSYQVLATEGYQSSGSSNVTW 212

RESULT 11
ID Q6TLP3_9BACT PRELIMINARY; PRT; 214 AA.
AC Q6TLP3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Endo-1,4-beta-xylanase precursor (EC 3.2.1.8).
OS uncultured bacterium.
OC Bacteria; environmental samples.
OX NCBI_TaxID=77133;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14718652; DOI=10.1110/ps.03333504;
RA Palackal N., Brennan Y., Callen W.N., Dupree P., Frey G., Goubet F.,
RA Hazlewood G.P., Healey S., Kang Y.E., Kretz K.A., Lee E., Tan X.,
RA Tomlinson G.L., Verruto J., Wong V.W.K., Mathur E.J., Short J.M.,
RA Robertson D.E., Steer B.A.;
RT "An evolutionary route to xylanase process fitness.";
RL Protein Sci. 13:494-503(2004).
DR EMBL; AY394562; AAQ90180.2; -; Genomic_DNA.
DR HSSP; P09850; 1BCX.
DR SMR; Q6TLP3; 30-214.
DR GO; GO:0031176; P:endo-1,4-beta-xylanase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0045493; P:xylan catabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
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DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; UNKNOWN_1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Glycosidase; Hydrolase; Signal; Xylan degradation.
FT SIGNAL 1 29 Potential.
SQ SEQUENCE 214 AA; 23478 MW; 6FD1CB9BB66A5048 CRC64;

Query Match 79.9%; Score 935.5; DB 2; Length 214;
Best Local Similarity 80.4%; Pred. No. 2.1e-67;
Matches 172; Conservative 13; Mismatches 28; Indels 1; Gaps 1;

Qy 1 MFKFKNPLVGLSALMSISLFSATASAASTDYQWNTDGGGINVAVNGSGGYSVNMNSN 59
Db 1 MFKSSKLLTVVLAASMSFGFFASTSNA--TDYQWNTDGGGTNAVNGSGGYSVMS 60

Qy 60 NTGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLYTGWTRSPLEIYVVDVDSWGTYRPT 119
Db 61 NCGNFVVGKWTGTSATRVINYNAGAPSPGNGYLYGWTRNSLIYVVDVDSWGTYRPT 120

Qy 120 GTYKGTVKS DGTGYDIYTTTTRYNAPSIDGRTTFTQYWSVRQSKRPTGNSNATITFSNHVN 179
Db 121 GTYKGTVTS DGTGYDIYTTTTRTNAPSIDGNNTTFTQFWSVRQSKRPITGNTNTITFSNHVN 180

Qy 180 AWKSHGMNLSNWAYOVNATEGYQSSGSSNVTW 213
Db 181 AWKSGMNLGSSNSYQVLATEGYQSSGYSNVTW 214

RESULT 12
XNA_BACST STANDARD; PRT; 210 AA.
AC P45705;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) (Xylanase A) (1,4-
DE beta-D-xylan xylanohydrolase A).
DE Name=xynA;
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=No. 236;
RA Cho S., Choi Y.;
RT "Nucleotide sequence analysis of an endo-xylanase gene (xynA) from
RT Bacillus stearothermophilus.";
RL J. Microbiol. Biotechnol. 5:117-124(1995).
RN [2]
RP SEQUENCE REVISION.
RA Cho S., Choi Y.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -! CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -! PATHWAY: Xylan degradation.
CC -! SIMILARITY: Belongs to the glycosyl hydrolase 11 (cellulase G)
CC family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; U15985; AAB72117.1; -; Genomic_DNA.
DR HSSP; P09850; 1XNB.
DR SMR; P45705; 24-210.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PR00457; GLHYDRLASE11.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Glycosidase; Hydrolase; Signal; Xylan degradation.
FT SIGNAL 1 19 Potential.
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FT CHAIN 20 210 Endo-1,4-beta-xylanase A.  
 FT ACT\_SITE 104 104 Nucleophile (By similarity).  
 FT ACT\_SITE 197 197 Proton donor (By similarity).  
 SQ SEQUENCE 210 AA; 23221 MW; 3190CF74C34AAB45 CRC64;

Query Match 79.4%; Score 930; DB 1; Length 210;  
 Best Local Similarity 80.6%; Pred. No. 5.6e-67;  
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QY 3 KFKQNFVGLSAAALMSISLFSATASASTDYQWNTDGGGVNAGVNGSGGNYSVNWSN 62  
 DB 2 KKKKQMLTLLTATSMISFLGATSSAA-TDYQWNTDGGGVNAGVNGSGGNYSVTWQNTG 60

QY 63 NFVVGKGTGTPFTINTYNAGVWAPNGNGYLTLGWTRSPLEIYYVVDVDSWGTYRPTG 122  
 DB 61 NFVVGKGTGTPFTINTYNAGVWAPNGNGYLTLGWTRSPLEIYYVVDVDSWGTYRPTG 120

QY 123 KGTVKSDDGTGYDIYTTTTRYNAPSIDGDRFTTQYWSVRQSKRPTGNSNATITFSNHVNA 182  
 DB 121 KGTVNSDDGTGYDIYTTTTRYNAPSIDGQ-TFQQFWSVRQSKRPTGNSNATITFSNHVNA 179

QY 183 SHGMNLGSSWAYQVMATGYSQSSGSSNVTW 213  
 DB 180 SKGMNLGSSWAYQVLAATEGYSQSSGSSNVTW 210

RESULT 13  
 Q43993\_AERPU PRELIMINARY; PRT; 211 AA.  
 AC Q43993.  
 DT 01-NOV-1996 (TREMELrel. 01, Created)  
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)  
 DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)  
 DE Xylanase I precursor.  
 GN Name=xynA;  
 OS Aeromonas punctata (Aeromonas caviae).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;  
 OC Aeromonadaceae; Aeromonas.  
 OX NCBI\_TaxID=648;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=ME-1; TISSUE=Gut content of silk worm;  
 RA Kubata K.B., Suzuki T., Horitsu H., Kawai K., Takamizawa K.;  
 RT "Xylanase I of Aeromonas caviae ME-1 isolated from the intestine of a  
 RT herbivorous insect (Samia cynthia pryeri).";  
 RL Biosci. Biotechnol. Biochem. 56:1463-1464 (1992).  
 RN [2]

RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=ME-1; TISSUE=Gut content of silk worm;  
 RA Suzuki T., Itoh Y., Naito H., Kubata K.B., Horitsu H., Takamizawa K.,  
 RA Kawai K.;  
 RT "Molecular cloning of the xynA gene encoding an endo-xylanase  
 RT 1) of Aeromonas caviae ME-1.";  
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; D32065; BAA06837.1; -; Genomic\_DNA.  
 DR HSSP; P09850; 1XNB.  
 DR SMR; Q43993; 25-211.  
 DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . . ; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR GO; GO:0045493; P:xylan catabolism; IEA.  
 DR GO; GO:0004543; P:xylan catabolism; IEA.  
 DR InterPro; IPR001137; Glyco\_hydro\_11.  
 DR Pfam; PF00457; Glyco\_hydro\_11.  
 DR PRINTS; PR00911; GLYDRLASE11.  
 DR PROSITE; PS00776; GLYCOSYL\_HYDROL\_F11\_1; UNKNOWN\_1.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 KW Signal; Xylan degradation.  
 FT SIGNAL 1 28 Potential.  
 FT CHAIN 29 211 xylanase I.  
 EQ SEQUENCE 211 AA; 23136 MW; F9E30403EB935E49 CRC64;

Query Match 79.3%; Score 929; DB 2; Length 211;  
 Best Local Similarity 79.3%; Pred. No. 6.8e-67;  
 Matches 169; Conservative 18; Mismatches 24; Indels 2; Gaps 2;

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 DB 1 MPKFGKMLTAVVLAASMSFGVFAATSSAA-TDYQWNTDGGGVNAGVNGSGGNYSVWQW 59

QY 61 TGNFVVGKGTGTPFTINTYNAGVWAPNGNGYLTLGWTRSPLEIYYVVDVDSWGTYRPTG 120  
 DB 60 TGNFVVGKGTGTPFTINTYNAGVWAPNGNGYLTLGWTRSPLEIYYVVDVDSWGTYRPTG 119

QY 121 TYKGTVKSDDGTGYDIYTTTTRYNAPSIDGDRFTTQYWSVRQSKRPTGNSNATITFSNHVNA 180  
 DB 120 TYKGTVNSDDGTGYDIYTTTTRYNAPSIDGQ-TFQQFWSVRQSKRPTGNSNATITFSNHVNA 178

QY 181 WKSHGMNLGSSWAYQVMATGYSQSSGSSNVTW 213  
 DB 179 WPSKGMNLGSSWSYQVMATGYSQSSGSSNVTW 211

RESULT 14  
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 AC Q71S35.  
 DT 05-JUL-2004 (TREMELrel. 27, Created)  
 DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)  
 DE Xylanase.  
 OS Bacillus firmus.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1399;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=K-1;  
 RA Chuensumran U., Ratanakhanokchai K., Cheevadhanarak S.;  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF317713; AAQ14588.1; -; Genomic\_DNA.  
 DR HSSP; P09850; 1BCX.  
 DR SMR; Q71S35; 27-210.  
 DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . . ; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR GO; GO:0045493; P:xylan catabolism; IEA.  
 DR InterPro; IPR001137; Glyco\_hydro\_11.  
 DR Pfam; PF00457; Glyco\_hydro\_11.  
 DR PRINTS; PR00911; GLYDRLASE11.  
 DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
 KW Xylan degradation.  
 SQ SEQUENCE 210 AA; 23313 MW; AC4BA5DD5D67A1B2 CRC64;

Query Match 73.8%; Score 864.5; DB 2; Length 210;  
 Best Local Similarity 74.2%; Pred. No. 1.1e-61;  
 Matches 158; Conservative 19; Mismatches 33; Indels 3; Gaps 2;

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 DB 1 MPKFTVKLVTVIAATISFCLSAVPA--NTYQWYWDGGGVNATNGPGGNYSVTW 58

QY 61 TGNFVVGKGTGTPFTINTYNAGVWAPNGNGYLTLGWTRSPLEIYYVVDVDSWGTYRPTG 120  
 DB 59 TGNFVVGKGTGTPFTINTYNAGVWAPNGNGYLTLGWTRSPLEIYYVVDVDSWGTYRPTG 118

QY 121 TYKGTVKSDDGTGYDIYTTTTRYNAPSIDGDRFTTQYWSVRQSKRPTGNSNATITFSNHVNA 180  
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QY 181 WKSHGMNLGSSWAYQVMATGYSQSSGSSNVTW 213  
 DB 178 WRNAGMNLGSSWSYQVLAATEGYSQSSGSSNVTW 210

RESULT 15  
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 ID Q9KEF3\_BACHD PRELIMINARY;  
 AC Q9KEF3;  
 DT 01-OCT-2000 (TREMELrel. 15, Created)

01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
13-SEP-2005 (TReMBLrel. 31, Last annotation update)  
Name=xyn11A; OrderedLocusNames=BH0899;  
Bacillus halodurans.  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
NCBI\_TaxID=86665;  
(1)  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=C-125 / JCM 9153;  
RC MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;  
RX Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,  
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,  
RA Horikoshi K.;  
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus  
halodurans and genomic sequence comparison with Bacillus subtilis.";  
RL Nucleic Acids Res. 28:4317-4331 (2000).  
(2)  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=MIR32;  
RC MEDLINE=22269261; PubMed=12382115; DOI=10.1007/s00792-002-0269-4;  
RX Martinez M.A., Delgado O.D., Breccia J.D., Baigori M.D., Sineriz F.;  
RA "Revision of the taxonomic position of the xylanolytic Bacillus sp.  
MIR32 reidentified as Bacillus halodurans and plasmid-mediated  
RT transformation of B. halodurans.";  
RL Extremophiles 6:391-395 (2002).  
(3)  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=MIR32;  
RC Martinez M.A., Delgado O.D., Breccia J.D., Sineriz F.;  
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BA000004; BAB04618.1; -; Genomic DNA.  
DR EMBL; AY170624; AAO12276.1; -; Genomic DNA.  
DR PIR; C83762; C83762.  
DR HSSP; P09850; 1XNB.  
DR SMR; Q9KEF3; 27-210.  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.  
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
DR InterPro; IPR001137; Glyco\_hydro\_11.  
DR Pfam; PF00457; Glyco\_hydro\_11; 1.  
DR PRINTS; PR00911; GLYDRLASE11.  
DR PROSITE; PS00777; GLYCOSYL\_HYDROL\_F11\_2; 1.  
KW Complete proteome; Hydrolase.  
SQ SEQUENCE 210 AA; 23313 MW; AC4BA5DD5D67A1B2 CRC64;  
  
Query Match 73.8%; Score 864.5; DB 2; Length 210;  
Best Local Similarity 74.2%; Pred. No. 1.1e-61;  
Matches 158; Conservative 19; Mismatches 33; Indels 3; Gaps 2;  
  
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Db 59 TGNFVVGKWEIGSPNRTIHYNAGVWEPSPGNGYLYGWTRNQLIYVVDVNWGTYRPTG 118  
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Db 119 THRGTVSDGGTYDIYITTRNAPSIDGTQ--TFQQFWSVRSKRPTGNNVSIITFSNVNA 177  
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QY 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213  
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Db 178 WRNAGNIGSSWSYQVLATEGYQSSGRSNVTW 210  
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Search completed: February 3, 2006, 09:17:54  
Job time : 109 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 3, 2006, 09:18:52 ; Search time 30 Seconds  
(without alignments)  
586.997 Million cell updates/sec

Title: US-10-626-583-5

Perfect score: 1171

Sequence: 1 MFKEKKNFLVGLSAAALMSIS.....YQVMATEGYQSSGSSNTVTW 213

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

- 1: /cgn2\_6/ptodata/1/iaa/5\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1168	99.7	213	2	US-09-570-856B-1
2	1168	99.7	213	2	US-09-570-856B-13
3	1141	97.4	208	1	US-08-315-695-21
4	1130	96.5	213	1	US-08-104-445-3
5	1041	88.9	185	1	US-08-044-621D-37
6	1041	88.9	185	1	US-08-709-912-5
7	1041	88.9	185	1	US-09-047-370-5
8	1038	88.6	185	1	US-08-044-621D-36
9	1038	88.6	185	1	US-08-709-912-3
10	1038	88.6	185	1	US-09-047-370-3
11	987	84.3	185	2	US-09-570-856B-5
12	984	84.0	185	2	US-09-570-856B-9
13	979	83.6	185	2	US-09-570-856B-7
14	977	83.4	185	2	US-09-570-856B-4
15	976	83.3	185	2	US-09-570-856B-6
16	974	83.2	185	2	US-09-570-856B-3
17	955	81.6	185	2	US-09-570-856B-10
18	955	81.6	211	1	US-08-575-964-1
19	955	81.6	211	1	US-08-963-500-1
20	951	81.2	185	2	US-09-570-856B-12
21	933	79.7	185	2	US-09-570-856B-8
22	920	78.6	185	2	US-09-570-856B-11
23	640.5	54.7	189	1	US-08-709-912-13
24	640.5	54.7	189	1	US-09-047-370-13
25	637	54.4	240	2	US-09-570-856B-16
26	636	54.3	344	1	US-08-468-812-2
27	636	54.3	344	2	US-08-590-563-2

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29	636	54.3	344	2	US-09-235-832-2	Sequence 2, Appli
30	635	54.2	216	1	US-08-315-695-20	Sequence 20, Appli
31	627.5	53.6	200	1	US-07-744-570B-2	Sequence 2, Appli
32	625.5	53.4	191	1	US-08-044-621D-35	Sequence 35, Appli
33	618.5	52.8	191	1	US-08-709-912-11	Sequence 11, Appli
34	618.5	52.8	191	1	US-09-047-370-11	Sequence 11, Appli
35	594	50.7	206	1	US-08-315-695-19	Sequence 19, Appli
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37	594	50.7	335	2	US-09-570-856B-15	Sequence 15, Appli
38	587	50.1	191	1	US-08-709-912-10	Sequence 10, Appli
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40	585.5	50.0	230	2	US-08-768-373-4	Sequence 4, Appli
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42	583.5	49.8	225	1	US-08-290-979A-8	Sequence 8, Appli
43	579	49.4	189	1	US-08-044-621D-33	Sequence 33, Appli
44	573.5	49.0	225	2	US-09-570-856B-26	Sequence 26, Appli
45	572	48.8	189	1	US-08-709-912-12	Sequence 12, Appli

ALIGNMENTS

RESULT 1

US-09-570-856B-1  
; Sequence 1, Application US/09570856B  
; Patent No. 6682923  
; GENERAL INFORMATION:  
; APPLICANT: Bentzien, Joerg M  
; APPLICANT: Dabivat, Basil I  
; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE  
; FILE REFERENCE: A-67478-1/RFT/RMS/RMK  
; CURRENT APPLICATION NUMBER: US/09/570.856B  
; CURRENT FILING DATE: 2002-04-15  
; PRIOR APPLICATION NUMBER: US 60/133,714  
; PRIOR FILING DATE: 1999-05-12  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 1  
; LENGTH: 213  
; TYPE: PRT  
; ORGANISM: Bacillus circulans  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: (1)..(28)  
; OTHER INFORMATION:  
; FEATURE:  
; NAME/KEY: mat\_peptide  
; LOCATION: (29)..()  
; OTHER INFORMATION:  
US-09-570-856B-1

Query Match	99.7%	Score 1168;	DB 2;	Length 213;
Best Local Similarity	99.5%	Pred. No. 6.3e-98;		
Matches 212;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MFKEKKNFLVGLSAAALMSISLFSATAAASDYQNQNTDGGIVNAVNGSGNTSVNWSN	60	
Db	1	MFKEKKNFLVGLSAAALMSISLFSATAAASDYQNQNTDGGIVNAVNGSGNTSVNWSN	60	
Qy	61	TGNFVVGKGTGTPFRFTINYNAGVAPNGVNGYLTLYGWTSPLEIYYVVDVSWGTYRPTG	120	
Db	61	TGNFVVGKGTGTPFRFTINYNAGVAPNGVNGYLTLYGWTSPLEIYYVVDVSWGTYRPTG	120	
Qy	121	TYKGTVKSDDGTGYDIYTTTTRYNAPSIDGDRFTTFTQYMSVROSKEPTGSGNATITFSNHVNA	180	
Db	121	TYKGTVKSDDGTGYDIYTTTTRYNAPSIDGDRFTTFTQYMSVROSKEPTGSGNATITFSNHVNA	180	
Qy	181	WKSHGMNLGNSWAYQVNMATEGYQSSGSSNTVTW	213	
Db	181	WKSHGMNLGNSWAYQVNMATEGYQSSGSSNTVTW	213	





```
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5306633man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 583-179-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 213 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-104-445-3

Query Match      96.5%; Score 1130; DB 1; Length 213;
Best Local Similarity 95.3%; Pred. No. 1.7e-94;
Matches 203; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 MFKFKFLVLGLSALMSISLPSATASASTDYQWQNTDGGGINVAVNGSGGNYSVWNSN 60
DB 1 MFKFKFLVLGLTAAFMSISLPSATASAGTDYQWQNTDGGGINVAVNGSGGNYSVWNSN 60
QY 61 TGNFVVGKGTGTSPPRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTG 120
DB 61 TGNFVVGKGTGTSPPRTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTG 120
QY 121 TYGTVKSDGGTYDIYTTTRYNAPSIDGRTTFTQYWSVRSKRTGSGNATITFSNHVNA 180
DB 121 TYGTVKSDGGTYDIYTTTRYNAPSIDGNTTFTQYWSVRSKRTGSGNATITFSNHVNA 180
QY 181 WKSHGMNLGNWAYQVMALEGYQSSGSSNVTW 213
DB 181 WKSHGMNLGNWAYQVMALEGYKSSGSSNVTW 213

RESULT 5
US-08-044-621D-37
; Sequence 37, Application US/08044621D
; Patent No. 5405769
; GENERAL INFORMATION:
; APPLICANT: Warren W. Wakarchuk
; APPLICANT: Wing L. Sung
; APPLICANT: Makoto Yaguchi
; APPLICANT: Robert L. Campbell
; APPLICANT: David R. Rose
; TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS
; TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; STREET: Suite 2600, 160 Elgin Street
; CITY: Ottawa
; STATE: Ontario
; COUNTRY: Canada
; ZIP: K1P 1C3
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 in., 360KB storage
; COMPUTER: IBM PC
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/044,621D
; FILING DATE: April 8, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Judy A. Erratt
; REGISTRATION NUMBER: 34,076
; REFERENCE/DOCKET NUMBER: 08-863796
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 613-786-0199
; TELEFAX: 613-563-9869
; TELEX:
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185
; TYPE: Amino Acid
; STRANDEDNESS: No. 5405769 Relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus subtilis
; IMMEDIATE SOURCE:
; POSITION IN GENOME:
; FEATURE:
; PUBLICATION INFORMATION:
; AUTHORS: Paice M.G., Bourbonnais R., Desrochers
; AUTHORS: M., Jurasek L., & Yaguchi M.
; TITLE:
; JOURNAL: Arch. Microbiol.
; VOLUME: 144
; ISSUE:
; PAGES: 201-206
; DATE: 1986
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
; US-08-044-621D-37

Query Match      88.9%; Score 1041; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.6e-86;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 ASTDYQWNTDGGGINVAVNGSGGNYSVWNSNTGNFVVGKGTGSGPRTINYNAGVWAP 88
DB 1 ASTDYQWNTDGGGINVAVNGSGGNYSVWNSNTGNFVVGKGTGSGPRTINYNAGVWAP 60
QY 89 NNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTGTYGTVKSDGGTYDIYTTTRYNAPSIDG 148
DB 61 NNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTGTYGTVKSDGGTYDIYTTTRYNAPSIDG 120
QY 149 DRTTFTQYWSVRSKRTGSGNATITFSNHVNAWKSHGMNLGNWAYQVMALEGYQSSGSS 208
DB 121 DRTTFTQYWSVRSKRTGSGNATITFSNHVNAWKSHGMNLGNWAYQVMALEGYQSSGSS 180
QY 209 NVTW 213
DB 181 NVTW 185

RESULT 6
US-08-709-912-5
; Sequence 5, Application US/08709912
; Patent No. 5759840
; GENERAL INFORMATION:
; APPLICANT: Sung Dr., Wing L
; APPLICANT: Yaguchi Dr., Makoto
; APPLICANT: Ishikawa Dr., Kazuhiko
; TITLE OF INVENTION: Modification of xylanase to improve
; TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
; TITLE OF INVENTION: Thermostability
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
; STREET: 277 Park Ave.
; CITY: New York
; STATE: New York
```

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; COUNTRY: USA
; ZIP: 10172-0194
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,912
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Olsen Mr, Warren E
; REGISTRATION NUMBER: 27290
; REFERENCE/DOCKET NUMBER: 1039.2000
; TELEPHONE: (212) 758-2400
; TELEFAX: (212) 758-2982
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORGANISM: Bacillus subtilis
; PUBLICATION INFORMATION:
; AUTHORS: Parce, M.G.
; AUTHORS: Bourbonnais, R
; AUTHORS: Desrochers, M
; AUTHORS: Jurasek, L
; AUTHORS: Yaguchi, M
; JOURNAL: Arch. Microbiol.
; VOLUME: 144
; PAGES: 201-206
; DATE: 1986
;
; US-08-709-912-5
;
; Query Match 88.9%; Score 1041; DB 1; Length 185;
; Best Local Similarity 100.0%; Pred. No. 1.6e-86;
; Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 29 ASTDYQNWTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPPTTINYNAGVWAP 88
; DB 1 ASTDYQNWTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPPTTINYNAGVWAP 60
;
; QY 89 NNGYLTLYGWTRSPLEIYYVVDWSGTYRPTGTYKGTGKSDGGTYDIYTTTRYNAPSIDG 148
; DB 61 NNGYLTLYGWTRSPLEIYYVVDWSGTYRPTGTYKGTGKSDGGTYDIYTTTRYNAPSIDG 120
;
; QY 149 DRTTFTQWSVRQSKRPTGSGNATITFSNHNVAWSKSHGNLGSNWAYQVMATEGYQSSGSS 208
; DB 121 DRTTFTQWSVRQSKRPTGSGNATITFSNHNVAWSKSHGNLGSNWAYQVMATEGYQSSGSS 180
;
; QY 209 NVTVM 213
; DB 181 NVTVM 185
;
; RESULT 7
; US-09-047-370-5
; Sequence 5, Application US/09047370
; Patent No. 5866408
; GENERAL INFORMATION:
; APPLICANT: Sung Dr., Wing L
; APPLICANT: Yaguchi Dr., Makoto
; APPLICANT: Ishikawa Dr., Kazuhiko
; TITLE OF INVENTION: Modification of xylanase to improve
; TITLE OF INVENTION: Thermophilicity, Alkalophilicity and

```

```

; TITLE OF INVENTION: Thermostability
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
; STREET: 277 Park Ave.
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10172-0194
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/047,370
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/709,912
; FILING DATE: 09-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Olsen Mr, Warren E
; REGISTRATION NUMBER: 27290
; REFERENCE/DOCKET NUMBER: 1039.2000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-2400
; TELEFAX: (212) 758-2982
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORGANISM: Bacillus subtilis
; PUBLICATION INFORMATION:
; AUTHORS: Parce, M.G.
; AUTHORS: Bourbonnais, R
; AUTHORS: Desrochers, M
; AUTHORS: Jurasek, L
; AUTHORS: Yaguchi, M
; JOURNAL: Arch. Microbiol.
; VOLUME: 144
; PAGES: 201-206
; DATE: 1986
;
; US-09-047-370-5
;
; Query Match 88.9%; Score 1041; DB 1; Length 185;
; Best Local Similarity 100.0%; Pred. No. 1.6e-86;
; Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 29 ASTDYQNWTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPPTTINYNAGVWAP 88
; DB 1 ASTDYQNWTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPPTTINYNAGVWAP 60
;
; QY 89 NNGYLTLYGWTRSPLEIYYVVDWSGTYRPTGTYKGTGKSDGGTYDIYTTTRYNAPSIDG 148
; DB 61 NNGYLTLYGWTRSPLEIYYVVDWSGTYRPTGTYKGTGKSDGGTYDIYTTTRYNAPSIDG 120
;
; QY 149 DRTTFTQWSVRQSKRPTGSGNATITFSNHNVAWSKSHGNLGSNWAYQVMATEGYQSSGSS 208
; DB 121 DRTTFTQWSVRQSKRPTGSGNATITFSNHNVAWSKSHGNLGSNWAYQVMATEGYQSSGSS 180
;
; QY 209 NVTVM 213
; DB 181 NVTVM 185

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RESULT 8  
US-08-044-621D-36  
; Sequence 36, Application US/08044621D  
; Patent No. 5405769  
; GENERAL INFORMATION:  
; APPLICANT: Warren W. Wakarchuk  
; APPLICANT: Wing L. Sung  
; APPLICANT: Makoto Yaguchi  
; APPLICANT: Robert L. Campbell  
; APPLICANT: David R. Rose  
; TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS  
; TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Gowling, Strathly & Henderson  
; STREET: Suite 2600, 160 Elgin Street  
; CITY: Ottawa  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: K1P 1C3  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 in., 360KB storage  
; COMPUTER: IBM PC  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/044,621D  
; FILING DATE: April 8, 1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Judy A. Erratt  
; REGISTRATION NUMBER: 34,076  
; REFERENCE/DOCKET NUMBER: 08-863796  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 613-786-0199  
; TELEFAX: 613-563-9869  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 36:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 185  
; TYPE: Amino Acid  
; STRANDEDNESS: No. 5405769 Relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; DESCRIPTION: protein  
; HYPOTHETICAL: No  
; ANTI-SENSE: No  
; FRAGMENT TYPE: No  
; ORIGINAL SOURCE:  
; ORGANISM: Bacillus circulans  
; IMMEDIATE SOURCE:  
; POSITION IN GENOME:  
; FEATURE:  
; PUBLICATION INFORMATION:  
; AUTHORS: Yang R.C.A., MacKenzie C.R. & Narang  
; AUTHORS: R.A.  
; TITLE:  
; JOURNAL: Nucleic Acids Res.  
; VOLUME: 16  
; ISSUE:  
; PAGES: 7187  
; DATE: 1988  
; DOCUMENT NUMBER:  
; FILING DATE:  
; PUBLICATION DATE:  
; RELEVANT RESIDUES IN SEQ ID NO:  
US-08-044-621D-36

Query Match 88.6%; Score 1038; DB 1; Length 185;  
Best Local Similarity 99.5%; Pred. No. 3e-86;

Matches 184; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 29 ASTDYQWQNTDGGGIVNAVNGSGGNYSVNWSNTGTFVVGKGTGSPRTTINYNAGVWAP 88  
DB 1 ASTDYQWQNTDGGGIVNAVNGSGGNYSVNWSNTGTFVVGKGTGSPRTTINYNAGVWAP 60  
QY 89 NGGYLTLYGWTRSPLEIYYVVDVDSNGTYRPTGTGTYKGTGKSDGGTYDITYTTRYNAPSIDG 148  
DB 61 NGGYLTLYGWTRSPLEIYYVVDVDSNGTYRPTGTGTYKGTGKSDGGTYDITYTTRYNAPSIDG 120  
QY 149 DRTTFTQYWSVRQSKRPTGSGNATITPSNHNVAWKGSHGNLGSNWAYQVMATEGYQSSGSS 208  
DB 121 DRTTFTQYWSVRQSKRPTGSGNATITPSNHNVAWKGSHGNLGSNWAYQVMATEGYQSSGSS 180  
QY 209 NVTWV 213  
DB 181 NVTWV 185  
RESULT 9  
US-08-709-912-3  
; Sequence 3, Application US/08709912  
; Patent No. 5759840  
; GENERAL INFORMATION:  
; APPLICANT: Sung Dr., Wing L  
; APPLICANT: Yaguchi Dr., Makoto  
; APPLICANT: Ishikawa Dr., Kazuhiko  
; TITLE OF INVENTION: Modification of Xylanase to Improve  
; TITLE OF INVENTION: Thermophilicity, Alkalophilicity and  
; TITLE OF INVENTION: Thermostability  
; NUMBER OF SEQUENCES: 54  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto  
; STREET: 277 Park Ave.  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10172-0194  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/709,912  
; FILING DATE: 09-SEP-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Olsen Mr, Warren E  
; REGISTRATION NUMBER: 27290  
; REFERENCE/DOCKET NUMBER: 1039.2000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 758-2400  
; TELEFAX: (212) 758-2982  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 185 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
; ORGANISM: Bacillus circulans  
; PUBLICATION INFORMATION:  
; AUTHORS: Yang, R.C.A.  
; AUTHORS: MacKenzie, C.R.  
; AUTHORS: Narang, S.A.  
; JOURNAL: Nucleic Acid Research  
; VOLUME: 16  
; PAGES: 7187

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f
US-08-709-912-3
DATE: 1988
US-08-709-912-3
Query Match      88.6%; Score 1038; DB 1; Length 185;
Best Local Similarity 99.5%; Pred. No. 3e-86;
Matches 184; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 29 ASTDYWQNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTTINYAGVWAP 88
Db 1 ASTDYWQNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTTINYAGVWAP 60

Qy 89 NNGYLTLYGWTRSPLEIYYVVDWSWGTYPRTGTGTYKGVKSDGGTYDIYTTTRYNAPSIDG 148
Db 61 NNGYLTLYGWTRSPLEIYYVVDWSWGTYPRTGTGTYKGVKSDGGTYDIYTTTRYNAPSIDG 120

Qy 149 DRTTFTQYWSVRQSKRPTGSGNATITFSNHNVAWSHGMLGNSNWAYQVMATEGYQSSGSS 208
Db 121 DRTTFTQYWSVRQSKRPTGSGNATITFTNHVNAWSHGMLGNSNWAYQVMATEGYQSSGSS 180

Qy 209 NVTVM 213
Db 181 NVTVM 185

RESULT 10
US-09-047-370-3
; Sequence 3, Application US/09047370
; Patent No. 586408
; GENERAL INFORMATION:
; APPLICANT: Sung Dr., Wing L
; APPLICANT: Yaguchi Dr., Makoto
; APPLICANT: Ishikawa Dr., Kazuhiko
; TITLE OF INVENTION: Modification of Xylanase to Improve
; TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
; TITLE OF INVENTION: Thermostability
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
; STREET: 277 Park Ave.
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10172-0194
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/047,370
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/709,912
; FILING DATE: 09-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Olsen Mr, Warren E
; REGISTRATION NUMBER: 27290
; REFERENCE/DOCKET NUMBER: 1039.2000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-2400
; TELEFAX: (212) 758-2982
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:

; ORGANISM: Bacillus circulans
; PUBLICATION INFORMATION:
; AUTHORS: Yang, R.C.A.
; AUTHORS: MacKenzie, C.R.
; JOURNAL: Nucleic Acid Research
; VOLUME: 16
; PAGES: 7187
; DATE: 1988
; US-09-047-370-3

Query Match      88.6%; Score 1038; DB 1; Length 185;
Best Local Similarity 99.5%; Pred. No. 3e-86;
Matches 184; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 29 ASTDYWQNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTTINYAGVWAP 88
Db 1 ASTDYWQNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTTINYAGVWAP 60

Qy 89 NNGYLTLYGWTRSPLEIYYVVDWSWGTYPRTGTGTYKGVKSDGGTYDIYTTTRYNAPSIDG 148
Db 61 NNGYLTLYGWTRSPLEIYYVVDWSWGTYPRTGTGTYKGVKSDGGTYDIYTTTRYNAPSIDG 120

Qy 149 DRTTFTQYWSVRQSKRPTGSGNATITFSNHNVAWSHGMLGNSNWAYQVMATEGYQSSGSS 208
Db 121 DRTTFTQYWSVRQSKRPTGSGNATITFTNHVNAWSHGMLGNSNWAYQVMATEGYQSSGSS 180

Qy 209 NVTVM 213
Db 181 NVTVM 185

RESULT 11
US-09-570-856B-5
; Sequence 5, Application US/09570856B
; Patent No. 6682923
; GENERAL INFORMATION:
; APPLICANT: Bentzien, Joerg M
; APPLICANT: Dahiyat, Basil I
; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
; FILE REFERENCE: A-67478-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/570,856B
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/133,714
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
; US-09-570-856B-5

Query Match      84.3%; Score 987; DB 2; Length 185;
Best Local Similarity 94.6%; Pred. No. 1.2e-81;
Matches 175; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 29 ASTDYWQNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTTINYAGVWAP 88
Db 1 ASTDYWQNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTTINYAGVWAP 60

Qy 89 NNGYLTLYGWTRSPLEIYYVVDWSWGTYPRTGTGTYKGVKSDGGTYDIYTTTRYNAPSIDG 148
Db 61 NNGYLTLYGWTRSPLEIYYVVDWSWGTYPRTGTGTYKGVKSDGGTYDIYTTTRYNAPSIDG 120

Qy 149 DRTTFTQYWSVRQSKRPTGSGNATITFSNHNVAWSHGMLGNSNWAYQVMATEGYQSSGSS 208
Db 121 DRTTFTQYWSVRQSKRPTGSGNATITFTNHVNAWSHGMLGNSNWAYQVMATEGYQSSGSS 180

Qy 209 NVTVM 213
Db 181 NVTVM 185
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Db      181 NVTW 185

RESULT 12
US-09-570-856B-9
; Sequence 9, Application US/09570856B
; Patent No. 6682923
; GENERAL INFORMATION:
; APPLICANT: Bentzien, Joerg M
; APPLICANT: Dahiyat, Bassil I
; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
; FILE REFERENCE: A-67478-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/570,856B
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/133,714
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-570-856B-9

Query Match      84.0%; Score 984; DB 2; Length 185;
Best Local Similarity 93.5%; Pred. No. 2.3e-81;
Matches 173; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy      29 ASTDYQWNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGTTGSPPTTINYNAGVWAP 88
      1 ASTDYQWNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGTTGSPPTTINYNAGVWAP 60

Qy      89 NNGGYLTLYGWTRSPLEIYYVVDWSGTYRPTGTGTYKGVKSDGGTYDIYTTTRYNAPSIDG 148
      61 NNGGYLTLYGWTRSPLEIYYVVDWSGTYRPTGTGTYKGVKSDGGTYDIYTTTRYNAPSIDG 120

Qy      149 DRTFTQYWSVRQSKRPTGSGNATITFNSHNVAWSKSHGNLGSNNWAYQVMATEGYQSSGSS 208
      121 DRTFTQYWSVRQSKRPTGSGNATITFNSHNVAWSKSHGNLGSNNWAYQVMATEGYQSSGSS 180

Qy      209 NVTW 213
      181 NVTW 185

RESULT 14
US-09-570-856B-4
; Sequence 4, Application US/09570856B
; Patent No. 6682923
; GENERAL INFORMATION:
; APPLICANT: Bentzien, Joerg M
; APPLICANT: Dahiyat, Bassil I
; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
; FILE REFERENCE: A-67478-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/570,856B
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/133,714
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-570-856B-4

Query Match      83.4%; Score 977; DB 2; Length 185;
Best Local Similarity 94.1%; Pred. No. 9.8e-81;
Matches 174; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy      29 ASTDYQWNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGTTGSPPTTINYNAGVWAP 88
      1 ASTDYQWNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGTTGSPPTTINYNAGVWAP 60

Qy      89 NNGGYLTLYGWTRSPLEIYYVVDWSGTYRPTGTGTYKGVKSDGGTYDIYTTTRYNAPSIDG 148
      61 NNGGYLTLYGWTRSPLEIYYVVDWSGTYRPTGTGTYKGVKSDGGTYDIYTTTRYNAPSIDG 120

Qy      149 DRTFTQYWSVRQSKRPTGSGNATITFNSHNVAWSKSHGNLGSNNWAYQVMATEGYQSSGSS 208
      121 DRTFTQYWSVRQSKRPTGSGNATITFNSHNVAWSKSHGNLGSNNWAYQVMATEGYQSSGSS 180

Qy      209 NVTW 213
      181 NVTW 185

RESULT 15
US-09-570-856B-6
; Sequence 6, Application US/09570856B
; Patent No. 6682923
; GENERAL INFORMATION:
; APPLICANT: Bentzien, Joerg M
; APPLICANT: Dahiyat, Bassil I
; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
; FILE REFERENCE: A-67478-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/570,856B
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-570-856B-7

Query Match      83.6%; Score 979; DB 2; Length 185;
Best Local Similarity 94.1%; Pred. No. 6.5e-81;
Matches 174; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy      29 ASTDYQWNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGTTGSPPTTINYNAGVWAP 88
      1 ASTDYQWNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGTTGSPPTTINYNAGVWAP 60

Qy      89 NNGGYLTLYGWTRSPLEIYYVVDWSGTYRPTGTGTYKGVKSDGGTYDIYTTTRYNAPSIDG 148
      61 NNGGYLTLYGWTRSPLEIYYVVDWSGTYRPTGTGTYKGVKSDGGTYDIYTTTRYNAPSIDG 120

Qy      149 DRTFTQYWSVRQSKRPTGSGNATITFNSHNVAWSKSHGNLGSNNWAYQVMATEGYQSSGSS 208
      121 DRTFTQYWSVRQSKRPTGSGNATITFNSHNVAWSKSHGNLGSNNWAYQVMATEGYQSSGSS 180

Qy      209 NVTW 213
      181 NVTW 185

RESULT 13
US-09-570-856B-7
; Sequence 7, Application US/09570856B
; Patent No. 6682923
; GENERAL INFORMATION:
; APPLICANT: Bentzien, Joerg M
; APPLICANT: Dahiyat, Bassil I
; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
; FILE REFERENCE: A-67478-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/570,856B
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/133,714
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-570-856B-7

Query Match      83.6%; Score 979; DB 2; Length 185;
Best Local Similarity 94.1%; Pred. No. 6.5e-81;
Matches 174; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
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! PRIOR APPLICATION NUMBER: US 60/133,714  
; PRIOR FILING DATE: 1999-05-12  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 185  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic  
US-09-570-856B-6

Query Match 83.3%; Score 976; DB 2; Length 185;  
Best Local Similarity 94.1%; Pred. No. 1.2e-80;  
Matches 174; Conservative 5; Mismatches 6; Indels 0; Gaps 0;  
  
Qy 29 ASTDYWQNWTDGGGIVNAVNGSGGNYSVNWSTGNTGNFVVGKWTTCGPPRTIYNAGYVAP 88  
Db 1 ASTDYWQNWTDGGGIVNAVNGSGGNYSVNWSTGNTGNFVVGKWTTCGPPRTIYNAGYVAP 60  
  
Qy 89 NNGYLTLYGWTRSPLEIYYVVDGNGTYRPTGTGTYKGTGKSDGGTYDIYTTTTRYNAPSIDG 148  
Db 61 NNGYLTLYGWTRSPLEIYYVVDGNGTYRPTGTGTYKGTGKSDGGTYDIYTTTTRYNAPSIDG 120  
  
Qy 149 DRTTFTQYWSYRQSKRPTGSGNATITFSNHNNAWKSHGNNLGSNNWAYQVMATEGYQSSGSS 208  
Db 121 DRTTFTQYWSYRQSKRPTGSGNATITFSNHNNAWKSHGNNLGSNNWAYQVMATEGYQSSGSS 180  
  
Qy 209 NVTW 213  
Db 181 NVTW 185

Search completed: February 3, 2006, 09:19:30  
Job time : 30 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 3, 2006, 09:23:48 ; Search time 180 Seconds  
(without alignments)  
494.431 Million cell updates/sec

Title: US-10-626-583-5

Perfect score: 1171

Sequence: 1 MFKKKKNFLVGLSAAALMSIS.....YQVMATEGYQSSGSSNTVTW 213

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1171	100.0	213	4	US-10-237-386-16
2	1171	100.0	213	5	US-10-626-583-5
3	1171	100.0	213	5	US-10-626-724-5
4	1168	99.7	213	4	US-10-237-386-17
5	1161	99.1	213	5	US-10-626-583-11
6	1161	99.1	213	5	US-10-626-724-11
7	1154	98.5	213	5	US-10-626-583-7
8	1154	98.5	213	5	US-10-626-724-7
9	1149	98.1	213	5	US-10-626-583-9
10	1149	98.1	213	5	US-10-626-724-9
11	1130	96.5	213	5	US-10-626-583-3
12	1130	96.5	213	5	US-10-626-724-3
13	1041	88.9	185	4	US-10-307-441-5
14	1041	88.9	185	4	US-10-237-386-1
15	1041	88.9	185	6	US-11-088-725A-32
16	1041	88.9	197	4	US-10-442-148A-10
17	1041	88.9	360	4	US-10-442-148A-11
18	1038	88.6	185	4	US-10-307-441-3
19	1038	88.6	185	6	US-11-088-725A-30
20	929	79.3	211	4	US-10-237-386-19
21	907.5	77.5	211	4	US-10-237-386-18
22	885	75.6	185	6	US-11-018-645-2
23	885	75.6	186	6	US-11-018-645-14
24	826.5	70.6	192	6	US-11-018-645-8
25	825	70.5	186	6	US-11-018-645-16
26	686.5	58.6	197	6	US-11-018-645-4
27	686.5	58.6	198	6	US-11-018-645-18

28	663.5	56.7	241	4	US-10-237-386-43	Sequence 43, Appl
29	659	56.3	240	4	US-10-237-386-42	Sequence 42, Appl
30	646	55.2	242	4	US-10-237-386-41	Sequence 41, Appl
31	645.5	55.1	239	4	US-10-237-386-40	Sequence 40, Appl
32	640.5	54.7	189	4	US-10-307-441-13	Sequence 13, Appl
33	640.5	54.7	189	6	US-11-088-725A-40	Sequence 40, Appl
34	636	54.3	344	3	US-09-770-621-2	Sequence 2, Appl
35	636	54.3	344	4	US-10-286-993-2	Sequence 2, Appl
36	627.5	53.6	191	6	US-11-088-725A-44	Sequence 44, Appl
37	622	53.1	228	4	US-10-237-386-39	Sequence 39, Appl
38	621	53.0	240	4	US-10-237-386-38	Sequence 38, Appl
39	618.5	52.8	191	4	US-10-307-441-11	Sequence 11, Appl
40	618.5	52.8	191	6	US-11-088-725A-39	Sequence 39, Appl
41	617.5	52.7	234	4	US-10-213-990-69	Sequence 69, Appl
42	587	50.1	191	4	US-10-307-441-10	Sequence 10, Appl
43	587	50.1	191	6	US-11-088-725A-38	Sequence 38, Appl
44	581	49.6	225	4	US-10-237-386-36	Sequence 36, Appl
45	573.5	49.0	189	4	US-10-307-441-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1

US-10-237-386-16

; Sequence 16, Application US/10237386

; Publication No. US20030180895A1

; GENERAL INFORMATION:

; APPLICANT: Danisco A/S

; APPLICANT: Sorensen, Ole

; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor

; FILE REFERENCE: 674509-2046

; CURRENT APPLICATION NUMBER: US/10/237,386

; CURRENT FILING DATE: 2002-12-06

; PRIOR APPLICATION NUMBER: PCT/IB01/00426

; PRIOR FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: GB 0005585.5

; PRIOR FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: GB 0015751.1

; PRIOR FILING DATE: 2000-06-27

; NUMBER OF SEQ ID NOS: 66

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 16

; LENGTH: 213

; TYPE: PRT

; ORGANISM: Bacillus subtilis

US-10-237-386-16

Query Match 100.0%; Score 1171; DB 4; Length 213;

Best Local Similarity 100.0%; Pred. No. 1.5e-96;

Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MFKKKKNFLVGLSAAALMSISLFSATASAASTDYQNMWTDGGGINVAVNGSGGNYSVNWSN	60
Db	1	MFKKKKNFLVGLSAAALMSISLFSATASAASTDYQNMWTDGGGINVAVNGSGGNYSVNWSN	60
Qy	61	TGNFVVGKGTGTPFRITINAGVWAPNGNGYLTLTGWTRSPLEIYYVVDSSWGTYRPTG	120
Db	61	TGNFVVGKGTGTPFRITINAGVWAPNGNGYLTLTGWTRSPLEIYYVVDSSWGTYRPTG	120
Qy	121	TYKGTGVSDDGTYYIYTRTRYNAPSIDGDRITFTQYWSVRSKRPTGSGNATITFSNHVNA	180
Db	121	TYKGTGVSDDGTYYIYTRTRYNAPSIDGDRITFTQYWSVRSKRPTGSGNATITFSNHVNA	180
Qy	181	WKSCHMNLGSNWAYQVMATEGYQSSGSSNTVTW	213
Db	181	WKSCHMNLGSNWAYQVMATEGYQSSGSSNTVTW	213

RESULT 2

US-10-626-583-5

; Sequence 5, Application US/10626583

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RESULT 4
US-10-237-386-17
; Sequence 17, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sibbesen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Bacillus circulans
US-10-237-386-17

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; ORGANISM: Bacillus circulans
US-10-237-386-17

Query Match          99.7%; Score 1168; DB 4; Length 213;
Best Local Similarity 99.5%; Pred. No. 2.8e-96;
Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0

Qy      1  MFKFKKNFLVGLGSAALMSISLFSATASAASTDYQWNWTDGGGI VNAVNGSGGNYSVNWSN 60
Db      1  MFKFKKNFLVGLGSAALMSISLFSATASAASTDYQWNWTDGGGI VNAVNGSGGNYSVNWSN 60

Qy      61  TGNFVVGKGWTTGSPRTINYNAGVWAPNGNGYLTLYGWTRSPRIEYVVDWSGTYRPTG 120
Db      61  TGNFVVGKGWTTGSPRTINYNAGVWAPNGNGYLTLYGWTRSPRIEYVVDWSGTYRPTG 120

Qy      121  TYKGTVKSDGGTYDIIYTTIRYNAPSIDGDRDTFTQYWSVRQSKPTGSGNATITFSNHVNA 180
Db      121  TYKGTVKSDGGTYDIIYTTIRYNAPSIDGDRDTFTQYWSVRQSKPTGSGNATITFTTNHVNA 180

Qy      181  WKSHGHNILGSNWAYQVMATEGYQSSGSSNTVTW 213
Db      181  WKSHGHNILGSNWAYQVMATEGYQSSGSSNTVTW 213

RESULT 5
US-10-626-583-11

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; Sequence 11, Application US/10626583
; Publication No. US20040234998A1
; GENERAL INFORMATION:
; APPLICANT: SIBBESEN, OLE
; APPLICANT: SORESEN, JENS FRISBAEK
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: 078883/0132
; CURRENT APPLICATION NUMBER: US/10/626,583
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US/09/869,155
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/IB99/02071
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: GB 9828599.2
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: GB 9907805.7
; PRIOR FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: GB 9908645.6
; PRIOR FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Mutant Xylanase
US-10-626-583-11

Query Match          99.1%; Score 1161; DB 5; Length 213;
Best Local Similarity 99.1%; Pred. No. 1.2e-95;
Matches 211; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFKFKNPLVGLSAAALMSISLFSATASAASTDYQWNTDGGGINVAVNGSGGNYSVNWSN 60
Db 1 MFKFKNPLVGLSAAALMSISLFSATASAASTDYQWNTDGGGINVAVNGSGGNYSVNWSN 60
Qy 61 TGNFVVGKWTGSPFRTINTNAGVWAPNGNGYLYLGYWTRSPLEIYYVDSWGTYRPTG 120
Db 61 TGNFVVGKWTGSPFRTINTNAGVWAPNGNGYLYLGYWTRSPLEIYYVDSWGTYRPTG 120
Qy 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGDRFTTQYWSVRSKRPTGSGNATITFSNHVNA 180
Db 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGDRFTTQYWSVRSKRPTGSGNATITFSNHVNA 180
Qy 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213
Db 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213

RESULT 7
US-10-626-583-7
; Sequence 7, Application US/10626583
; Publication No. US20040234998A1
; GENERAL INFORMATION:
; APPLICANT: SIBBESEN, OLE
; APPLICANT: SORESEN, JENS FRISBAEK
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: 078883/0132
; CURRENT APPLICATION NUMBER: US/10/626,583
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US/09/869,155
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/IB99/02071
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: GB 9828599.2
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: GB 9907805.7
; PRIOR FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: GB 9908645.6
; PRIOR FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Mutant Xylanase
US-10-626-583-7

Query Match          98.5%; Score 1154; DB 5; Length 213;
Best Local Similarity 98.1%; Pred. No. 4.9e-95;
Matches 209; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFKFKNPLVGLSAAALMSISLFSATASAASTDYQWNTDGGGINVAVNGSGGNYSVNWSN 60
Db 1 MFKFKNPLVGLSAAALMSISLFSATASAASTDYQWNTDGGGINVAVNGSGGNYSVNWSN 60
Qy 61 TGNFVVGKWTGSPFRTINTNAGVWAPNGNGYLYLGYWTRSPLEIYYVDSWGTYRPTG 120
Db 61 TGNFVVGKWTGSPFRTINTNAGVWAPNGNGYLYLGYWTRSPLEIYYVDSWGTYRPTG 120

; Sequence 11, Application US/10626724
; Publication No. US20050079573A1
; GENERAL INFORMATION:
; APPLICANT: SIBBESEN, OLE
; APPLICANT: SORESEN, JENS FRISBAEK
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: 078883/0132
; CURRENT APPLICATION NUMBER: US/10/626,724
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US/09/869,155
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: PCT/IB99/02071
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: GB 9828599.2
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: GB 9907805.7
; PRIOR FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: GB 9908645.6
; PRIOR FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Mutant Xylanase
US-10-626-724-11

Query Match          99.1%; Score 1161; DB 5; Length 213;
Best Local Similarity 99.1%; Pred. No. 1.2e-95;
Matches 211; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFKFKNPLVGLSAAALMSISLFSATASAASTDYQWNTDGGGINVAVNGSGGNYSVNWSN 60
Db 1 MFKFKNPLVGLSAAALMSISLFSATASAASTDYQWNTDGGGINVAVNGSGGNYSVNWSN 60
Qy 61 TGNFVVGKWTGSPFRTINTNAGVWAPNGNGYLYLGYWTRSPLEIYYVDSWGTYRPTG 120
Db 61 TGNFVVGKWTGSPFRTINTNAGVWAPNGNGYLYLGYWTRSPLEIYYVDSWGTYRPTG 120
Qy 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGDRFTTQYWSVRSKRPTGSGNATITFSNHVNA 180
Db 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGDRFTTQYWSVRSKRPTGSGNATITFSNHVNA 180
Qy 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213
Db 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213

RESULT 6
US-10-626-724-11
; Sequence 11, Application US/10626724
; Publication No. US20050079573A1
; GENERAL INFORMATION:
; APPLICANT: SIBBESEN, OLE
; APPLICANT: SORESEN, JENS FRISBAEK
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: 078883/0132
; CURRENT APPLICATION NUMBER: US/10/626,724
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US/09/869,155
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: PCT/IB99/02071
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: GB 9828599.2
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: GB 9907805.7
; PRIOR FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: GB 9908645.6
; PRIOR FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Mutant Xylanase
US-10-626-724-11
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Db 61 TGNFVVGKWTGSPFRTINYNAGWAPNGNGYLTLYGWTRSPLEIYYVVDWSGTYRPTG 120  
Qy 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGDRITFTQYMSVRSKRPSTGSNATITFSNHVNA 180  
Db 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGDRITFTQYMSVRSKRPSTGSNATITFSNHVNA 180  
Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213  
Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

## RESULT 8

US-10-626-724-7  
; Sequence 7, Application US/10626724  
; Publication No. US20050079573A1  
; GENERAL INFORMATION:  
; APPLICANT: SIBBESEN, OLE  
; APPLICANT: SORESEN, JENS FRISBAEK  
; TITLE OF INVENTION: PROTEINS  
; FILE REFERENCE: 078883/0132  
; CURRENT APPLICATION NUMBER: US/10/626,724  
; PRIOR FILING DATE: 2003-07-25  
; PRIOR FILING DATE: 2001-06-25  
; PRIOR FILING DATE: 2001-06-25  
; PRIOR FILING DATE: 1999-12-17  
; PRIOR FILING DATE: 1999-12-17  
; PRIOR FILING DATE: 1998-12-23  
; PRIOR FILING DATE: 1998-12-23  
; PRIOR FILING DATE: 1999-04-06  
; PRIOR FILING DATE: 1999-04-06  
; PRIOR FILING DATE: 1999-04-15  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 213  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Mutant Xylanase  
US-10-626-724-7

Query Match 98.5%; Score 1154; DB 5; Length 213;  
Best Local Similarity 98.1%; Pred. No. 4.9e-95;  
Matches 209; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 MFKFKNFLVGLSAAALMSISLFSATASASTDYQWNTDGGGIYNAVNGSGGNYSVNWSN 60  
Db 1 MFKFKNFLVGLSAAALMSISLFSATASASTDYQWNTDGGGIYNAVNGSGGNYSVNWSN 60  
Qy 61 TGNFVVGKWTGSPFRTINYNAGWAPNGNGYLTLYGWTRSPLEIYYVVDWSGTYRPTG 120  
Db 61 TGNFVVGKWTGSPFRTINYNAGWAPNGNGYLTLYGWTRSPLEIYYVVDWSGTYRPTG 120  
Qy 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGDRITFTQYMSVRSKRPSTGSNATITFSNHVNA 180  
Db 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGDRITFTQYMSVRSKRPSTGSNATITFSNHVNA 180  
Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213  
Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

## RESULT 9

US-10-626-583-9  
; Sequence 9, Application US/10626583  
; Publication No. US20040234998A1  
; GENERAL INFORMATION:  
; APPLICANT: SIBBESEN, OLE  
; APPLICANT: SORESEN, JENS FRISBAEK  
; TITLE OF INVENTION: PROTEINS  
; FILE REFERENCE: 078883/0132

; CURRENT APPLICATION NUMBER: US/10/626,583  
; CURRENT FILING DATE: 2003-07-25  
; PRIOR APPLICATION NUMBER: US/09/869,155  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: PCT/IB99/02071  
; PRIOR FILING DATE: 1999-12-17  
; PRIOR APPLICATION NUMBER: GB 9828599.2  
; PRIOR FILING DATE: 1998-12-23  
; PRIOR APPLICATION NUMBER: GB 9907805.7  
; PRIOR FILING DATE: 1999-04-06  
; PRIOR APPLICATION NUMBER: GB 9908645.6  
; PRIOR FILING DATE: 1999-04-15  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 213  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Mutant Xylanase  
US-10-626-583-9

Query Match 98.1%; Score 1149; DB 5; Length 213;  
Best Local Similarity 97.7%; Pred. No. 1.4e-94;  
Matches 208; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 MFKFKNFLVGLSAAALMSISLFSATASASTDYQWNTDGGGIYNAVNGSGGNYSVNWSN 60  
Db 1 MFKFKNFLVGLSAAALMSISLFSATASASTDYQWNTDGGGIYNAVNGSGGNYSVNWSN 60  
Qy 61 TGNFVVGKWTGSPFRTINYNAGWAPNGNGYLTLYGWTRSPLEIYYVVDWSGTYRPTG 120  
Db 61 TGNFVVGKWTGSPFRTINYNAGWAPNGNGYLTLYGWTRSPLEIYYVVDWSGTYRPTG 120  
Qy 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGDRITFTQYMSVRSKRPSTGSNATITFSNHVNA 180  
Db 121 TYKGTVKS DGGTYDIYITTRYNAPSIDGDRITFTQYMSVRSKRPSTGSNATITFSNHVNA 180  
Qy 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213  
Db 181 WKSHGMNLGSNWAYQVWATEGYQSSGSSNVTW 213

## RESULT 10

US-10-626-724-9  
; Sequence 9, Application US/10626724  
; Publication No. US20050079573A1  
; GENERAL INFORMATION:  
; APPLICANT: SIBBESEN, OLE  
; APPLICANT: SORESEN, JENS FRISBAEK  
; TITLE OF INVENTION: PROTEINS  
; FILE REFERENCE: 078883/0132  
; CURRENT APPLICATION NUMBER: US/10/626,724  
; CURRENT FILING DATE: 2003-07-25  
; PRIOR APPLICATION NUMBER: US/09/869,155  
; PRIOR FILING DATE: 2001-06-25  
; PRIOR APPLICATION NUMBER: PCT/IB99/02071  
; PRIOR FILING DATE: 1999-12-17  
; PRIOR APPLICATION NUMBER: GB 9828599.2  
; PRIOR FILING DATE: 1998-12-23  
; PRIOR APPLICATION NUMBER: GB 9907805.7  
; PRIOR FILING DATE: 1999-04-06  
; PRIOR APPLICATION NUMBER: GB 9908645.6  
; PRIOR FILING DATE: 1999-04-15  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 213  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: Mutant Xylanase  
US-10-626-724-9

Query Match 98.1%; Score 1149; DB 5; Length 213;  
Best Local Similarity 97.7%; Pred. No. 1.4e-94;  
Matches 208; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MFKFKKFLVGLSALMSISLFSATASASTDYQWNTDGGGINAVNGSGGNYSVNWSN 60  
Db 1 MFKFKKFLVGLSALMSISLFSATASASTDYQWNTDGGGINAVNGSGGNYSVNWSN 60  
Qy 61 TGNFVVGKWTGSPFRITNNAGWAPNGNGYLTLGWTRSPLEIYYVVDVDSWGTYRPTG 120  
Db 61 TGNFVVGKWTGSPFRITNNAGWAPNGNGYLTLGWTRSPLEIYYVVDVDSWGTYRPTG 120  
Qy 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGDRFTTQYWSVRSKPTGSNATITFSNHVNA 180  
Db 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGDRFTTQYWSVRSKPTGSNATITFSNHVNA 180  
Qy 181 WKSHGMNLGSNWAYQVVLATEGYKSSGSSNVTVM 213  
Db 181 WKSHGMNLGSNWAYQVVLATEGYKSSGSSNVTVM 213

## RESULT 11

US-10-626-583-3

; Sequence 3, Application US/10626583  
; Publication No. US20040234998A1  
; GENERAL INFORMATION:  
; APPLICANT: SIBBSEN, OLE  
; APPLICANT: SORESEN, JENS FRISBAEK  
; TITLE OF INVENTION: PROTEINS  
; FILE REFERENCE: 078883/0132  
; CURRENT APPLICATION NUMBER: US/10/626.583  
; CURRENT FILING DATE: 2003-07-25  
; PRIOR APPLICATION NUMBER: US/09/869,155  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: PCT/IB99/02071  
; PRIOR FILING DATE: 1999-12-17  
; PRIOR APPLICATION NUMBER: GB 9828599.2  
; PRIOR FILING DATE: 1998-12-23  
; PRIOR APPLICATION NUMBER: GB 9907805.7  
; PRIOR FILING DATE: 1999-04-06  
; PRIOR APPLICATION NUMBER: GB 9908645.6  
; PRIOR FILING DATE: 1999-04-15  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 213  
; TYPE: PRT  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Xylanase  
US-10-626-583-3

Query Match 96.5%; Score 1130; DB 5; Length 213;  
Best Local Similarity 95.3%; Pred. No. 6.9e-93;  
Matches 203; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MFKFKKFLVGLSALMSISLFSATASASTDYQWNTDGGGINAVNGSGGNYSVNWSN 60  
Db 1 MFKFKKFLVGLTAAFMISMSFSAAGTDYQWNTDGGGTAVNAVNGSGGNYSVNWSN 60  
Qy 61 TGNFVVGKWTGSPFRITNNAGWAPNGNGYLTLGWTRSPLEIYYVVDVDSWGTYRPTG 120  
Db 61 TGNFVVGKWTGSPFRITNNAGWAPNGNGYLTLGWTRSPLEIYYVVDVDSWGTYRPTG 120  
Qy 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGDRFTTQYWSVRSKPTGSNATITFSNHVNA 180  
Db 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGDRFTTQYWSVRSKPTGSNATITFSNHVNA 180  
Qy 181 WKSHGMNLGSNWAYQVVLATEGYKSSGSSNVTVM 213  
Db 181 WKSHGMNLGSNWAYQVVLATEGYKSSGSSNVTVM 213

Db 181 WKSHGMNLGSNWAYQVVLATEGYKSSGSSNVTVM 213

## RESULT 12

US-10-626-724-3  
; Sequence 3, Application US/10626724  
; Publication No. US20050079573A1  
; GENERAL INFORMATION:  
; APPLICANT: SIBBSEN, OLE  
; APPLICANT: SORESEN, JENS FRISBAEK  
; TITLE OF INVENTION: PROTEINS  
; FILE REFERENCE: 078883/0132  
; CURRENT APPLICATION NUMBER: US/10/626.724  
; CURRENT FILING DATE: 2003-07-25  
; PRIOR APPLICATION NUMBER: US/09/869,155  
; PRIOR FILING DATE: 2001-06-25  
; PRIOR APPLICATION NUMBER: PCT/IB99/02071  
; PRIOR FILING DATE: 1999-12-17  
; PRIOR APPLICATION NUMBER: GB 9828599.2  
; PRIOR FILING DATE: 1998-12-23  
; PRIOR APPLICATION NUMBER: GB 9907805.7  
; PRIOR FILING DATE: 1999-04-06  
; PRIOR APPLICATION NUMBER: GB 9908645.6  
; PRIOR FILING DATE: 1999-04-15  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 213  
; TYPE: PRT  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Xylanase  
US-10-626-724-3

Query Match 96.5%; Score 1130; DB 5; Length 213;  
Best Local Similarity 95.3%; Pred. No. 6.9e-93;  
Matches 203; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MFKFKKFLVGLSALMSISLFSATASASTDYQWNTDGGGINAVNGSGGNYSVNWSN 60  
Db 1 MFKFKKFLVGLTAAFMISMSFSAAGTDYQWNTDGGGTAVNAVNGSGGNYSVNWSN 60  
Qy 61 TGNFVVGKWTGSPFRITNNAGWAPNGNGYLTLGWTRSPLEIYYVVDVDSWGTYRPTG 120  
Db 61 TGNFVVGKWTGSPFRITNNAGWAPNGNGYLTLGWTRSPLEIYYVVDVDSWGTYRPTG 120  
Qy 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGDRFTTQYWSVRSKPTGSNATITFSNHVNA 180  
Db 121 TYKGTVKSDDGTYDIYTTTRYNAPSIDGDRFTTQYWSVRSKPTGSNATITFSNHVNA 180  
Qy 181 WKSHGMNLGSNWAYQVVLATEGYKSSGSSNVTVM 213  
Db 181 WKSHGMNLGSNWAYQVVLATEGYKSSGSSNVTVM 213

## RESULT 13

US-10-307-441-5  
; Sequence 5, Application US/10307441  
; Publication No. US20030166236A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNG, Wing L.  
; APPLICANT: National Research Council of Canada  
; TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity  
; TITLE OF INVENTION: and Alkalophilicity  
; FILE REFERENCE: 027367-5006US  
; CURRENT APPLICATION NUMBER: US/10/307,441  
; CURRENT FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: PCT/CA01/00769  
; PRIOR FILING DATE: 2001-05-31  
; PRIOR APPLICATION NUMBER: 60/213,803  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 5
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-307-441-5

Query Match      88.9%; Score 1041; DB 4; Length 185;
Best Local Similarity 100.0%; Pred. No. 5.3e-85;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 ASTDYQWQNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTTINYAGVWAP 88
Db 1 ASTDYQWQNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTTINYAGVWAP 60

Qy 89 NNGYLTLYGWTRSPLEIYYVVDWSGTYRPTGTYKGTGKSDGGTYDIYTTTRYNAPSIDG 148
Db 61 NNGYLTLYGWTRSPLEIYYVVDWSGTYRPTGTYKGTGKSDGGTYDIYTTTRYNAPSIDG 120

Qy 149 DRTTFTQWVSQRKPTGSGNATITFSNHVNAWKSHGNLGSNNWAYQVMATEGYQSSGSS 208
Db 121 DRTTFTQWVSQRKPTGSGNATITFSNHVNAWKSHGNLGSNNWAYQVMATEGYQSSGSS 180

Qy 209 NVTVM 213
Db 181 NVTVM 185

Query Match      88.9%; Score 1041; DB 4; Length 185;
Best Local Similarity 100.0%; Pred. No. 5.3e-85;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 14
US-10-237-386-1
; Sequence 1, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sibbensen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-237-386-1

Query Match      88.9%; Score 1041; DB 4; Length 185;
Best Local Similarity 100.0%; Pred. No. 5.3e-85;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 ASTDYQWQNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTTINYAGVWAP 88
Db 1 ASTDYQWQNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTTINYAGVWAP 60

Qy 89 NNGYLTLYGWTRSPLEIYYVVDWSGTYRPTGTYKGTGKSDGGTYDIYTTTRYNAPSIDG 148
Db 61 NNGYLTLYGWTRSPLEIYYVVDWSGTYRPTGTYKGTGKSDGGTYDIYTTTRYNAPSIDG 120

Qy 149 DRTTFTQWVSQRKPTGSGNATITFSNHVNAWKSHGNLGSNNWAYQVMATEGYQSSGSS 208
Db 121 DRTTFTQWVSQRKPTGSGNATITFSNHVNAWKSHGNLGSNNWAYQVMATEGYQSSGSS 180

Qy 209 NVTVM 213
Db 181 NVTVM 185
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RESULT 15
US-11-088-725A-32
; Sequence 32, Application US/11088725A
; Publication No. US20050214410A1
; GENERAL INFORMATION:
; APPLICANT: Iogen Bio-Products Corporation
; APPLICANT: White, Theresa C
; APPLICANT: Giroux, Genevieve R
; APPLICANT: Wallace, Katie E.A.
; TITLE OF INVENTION: Modified Xylanases Exhibiting Improved Expression
; FILE REFERENCE: Q80712
; CURRENT APPLICATION NUMBER: US/11/088,725A
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/556,061
; PRIOR FILING DATE: 2004-03-25
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-11-088-725A-32

Query Match      88.9%; Score 1041; DB 6; Length 185;
Best Local Similarity 100.0%; Pred. No. 5.3e-85;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 ASTDYQWQNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTTINYAGVWAP 88
Db 1 ASTDYQWQNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTTINYAGVWAP 60

Qy 89 NNGYLTLYGWTRSPLEIYYVVDWSGTYRPTGTYKGTGKSDGGTYDIYTTTRYNAPSIDG 148
Db 61 NNGYLTLYGWTRSPLEIYYVVDWSGTYRPTGTYKGTGKSDGGTYDIYTTTRYNAPSIDG 120

Qy 149 DRTTFTQWVSQRKPTGSGNATITFSNHVNAWKSHGNLGSNNWAYQVMATEGYQSSGSS 208
Db 121 DRTTFTQWVSQRKPTGSGNATITFSNHVNAWKSHGNLGSNNWAYQVMATEGYQSSGSS 180

Qy 209 NVTVM 213
Db 181 NVTVM 185

Search completed: February 3, 2006, 09:28:57
Job time : 180 secs
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 3, 2006, 09:24:33 ; Search time 10 Seconds  
(without alignments)  
249.595 Million cell updates/sec

Title: US-10-626-583-5

Perfect score: 1171

Sequence: 1 MFKEKKNFLVGLSAAALMSIS.....YQWATEGYQSSGSSNTVTW 213

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 88029 seqs, 11718060 residues

Total number of hits satisfying chosen parameters: 88029

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1171	100.0	213	6	US-10-517-939-188
2	1171	100.0	213	7	US-11-170-653-16
3	1168	99.7	213	6	US-10-517-939-224
4	1168	99.7	213	7	US-11-170-653-17
5	1104	94.3	213	6	US-10-517-939-230
6	1097	93.7	213	6	US-10-517-939-302
7	1041	88.9	185	7	US-11-170-653-1
8	953	81.4	211	6	US-10-517-939-198
9	933.5	79.7	214	6	US-10-517-939-158
10	929	79.3	211	7	US-11-170-653-19
11	927	79.2	210	6	US-10-517-939-208
12	907.5	77.5	211	7	US-11-170-653-18
13	886	75.7	189	6	US-10-517-939-190
14	873.5	74.6	184	6	US-10-517-939-252
15	844	72.1	189	6	US-10-517-939-380
16	834	71.2	189	6	US-10-517-939-378
17	826	70.5	189	6	US-10-517-939-376
18	710	60.6	222	6	US-10-517-939-168
19	687	58.7	445	6	US-10-517-939-368
20	669.5	57.2	225	6	US-10-517-939-172
21	663.5	56.7	241	7	US-11-170-653-43
22	659	56.3	240	7	US-11-170-653-42
23	658	56.2	361	6	US-10-517-939-212
24	647.5	55.3	355	6	US-10-517-939-206
25	646	55.2	242	7	US-11-170-653-41

ALIGNMENTS

RESULT 1

US-10-517-939-188  
; Sequence 188, Application US/10517939  
; Publication No. US20060003433A1

GENERAL INFORMATION:

- APPLICANT: Steer, Brian
- APPLICANT: Callen, Walter
- APPLICANT: Healey, Shaun
- APPLICANT: Hazlewood, Geoff
- APPLICANT: Wu, Di
- APPLICANT: Blum, David
- APPLICANT: Eteghalian, Alireza
- TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
- TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
- FILE REFERENCE: 564462007901
- CURRENT APPLICATION NUMBER: US/10/517,939
- CURRENT FILING DATE: 2004-12-13
- PRIOR APPLICATION NUMBER: PCT/US03/19153
- PRIOR FILING DATE: 2003-06-16
- PRIOR APPLICATION NUMBER: 60/389,299
- PRIOR FILING DATE: 2002-06-14
- NUMBER OF SEQ ID NOS: 380
- SOFTWARE: FastSeq for Windows Version 4.0
- SEQ ID NO 188
- LENGTH: 213
- TYPE: PRT
- ORGANISM: Unknown
- FEATURE:
- OTHER INFORMATION: Obtained from an environmental sample
- FEATURE:
- NAME/KEY: SIGNAL
- LOCATION: (1) ... (28)

Query Match 100.0%; Score 1171; DB 6; Length 213;

Best Local Similarity 100.0%; Pred. No. 7.6e-96; Indels 0; Gaps 0;  
Matches 213; Conservative 0; Mismatches 0;

Qy	1	MFKEKKNFLVGLSAAALMSISLFSATASAASTDYQWNTDGGGIYVAVNGSGGNTSVNWSN	60
Db	1	MFKEKKNFLVGLSAAALMSISLFSATASAASTDYQWNTDGGGIYVAVNGSGGNTSVNWSN	60
Qy	61	TGNFVVGKGTGTPPRTTINYNAGVWAPNGNGYLTLYGWTSPLEIYYVVDWSGTYRPTG	120
Db	61	TGNFVVGKGTGTPPRTTINYNAGVWAPNGNGYLTLYGWTSPLEIYYVVDWSGTYRPTG	120
Qy	121	TYKGTVKSDDGTYDITTTTRYNAPSIDGDRTTFTQYKSVROSKRPTGSNATITFSNHVNA	180

Db 121 TYKGTVKS DGGTYDIYTTTTRYNAPSIDGDRITFTQYMSVRQSKRPTGSNATITFSNHVNA 180

Qy 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213

Db 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213

RESULT 2

US-11-170-653-16

Sequence 16, Application US/11170653

Publication No. US20050271769A1

GENERAL INFORMATION:

APPLICANT: Danisco A/S

APPLICANT: Sibbesen, Ole

APPLICANT: Sorensen, Jens

TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor

FILE REFERENCE: 674509-2046

CURRENT APPLICATION NUMBER: US/11/170,653

CURRENT FILING DATE: 2005-06-23

PRIOR APPLICATION NUMBER: US/10/237,386

PRIOR FILING DATE: 2002-09-09

PRIOR APPLICATION NUMBER: PCT/IB01/00426

PRIOR FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: GB 0005585.5

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: GB 0015751.1

PRIOR FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 66

SOFTWARE: PatentIn version 3.0

SEQ ID NO 16

LENGTH: 213

TYPE: PRT

ORGANISM: Bacillus subtilis

US-11-170-653-16

Query Match 100.0%; Score 1171; DB 7; Length 213;

Best Local Similarity 100.0%; Pred. No. 7.6e-96;

Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKEKKNFLVGLSAAALMSISLFSATASAASTDYQWQNTDGGGI VNAVNGSGNYSVNWSN 60

Db 1 MFKEKKNFLVGLSAAALMSISLFSATASAASTDYQWQNTDGGGI VNAVNGSGNYSVNWSN 60

Qy 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLTLYGWTSPLEIYYVVDWSGTYRPTG 120

Db 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLTLYGWTSPLEIYYVVDWSGTYRPTG 120

Qy 121 TYKGTVKS DGGTYDIYTTTTRYNAPSIDGDRITFTQYMSVRQSKRPTGSNATITFSNHVNA 180

Db 121 TYKGTVKS DGGTYDIYTTTTRYNAPSIDGDRITFTQYMSVRQSKRPTGSNATITFSNHVNA 180

Qy 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213

Db 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213

RESULT 3

US-10-517-939-224

Sequence 224, Application US/10517939

Publication No. US20060003433A1

GENERAL INFORMATION:

APPLICANT: Steer, Brian

APPLICANT: Callen, Walter

APPLICANT: Healey, Shaun

APPLICANT: Hazlewood, Geoff

APPLICANT: Wu, Di

APPLICANT: Blum, David

APPLICANT: Esteghlalian, Alireza

TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM

FILE REFERENCE: 564462007901

CURRENT APPLICATION NUMBER: US/10/517,939

CURRENT FILING DATE: 2004-12-13

Qy 1 MFKEKKNFLVGLSAAALMSISLFSATASAASTDYQWQNTDGGGI VNAVNGSGNYSVNWSN 60

Db 1 MFKEKKNFLVGLSAAALMSISLFSATASAASTDYQWQNTDGGGI VNAVNGSGNYSVNWSN 60

Qy 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLTLYGWTSPLEIYYVVDWSGTYRPTG 120

Db 61 TGNFVVGKWTGSPFRTINYNAGVWAPNGNGYLTLYGWTSPLEIYYVVDWSGTYRPTG 120

Qy 121 TYKGTVKS DGGTYDIYTTTTRYNAPSIDGDRITFTQYMSVRQSKRPTGSNATITFSNHVNA 180

Db 121 TYKGTVKS DGGTYDIYTTTTRYNAPSIDGDRITFTQYMSVRQSKRPTGSNATITFSNHVNA 180

Qy 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213

Db 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW 213

RESULT 4

US-11-170-653-17

Sequence 17, Application US/11170653

Publication No. US20050271769A1

GENERAL INFORMATION:

APPLICANT: Danisco A/S

APPLICANT: Sibbesen, Ole

APPLICANT: Sorensen, Jens

TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor

FILE REFERENCE: 674509-2046

CURRENT APPLICATION NUMBER: US/11/170,653

CURRENT FILING DATE: 2005-06-23

PRIOR APPLICATION NUMBER: US/10/237,386

PRIOR FILING DATE: 2002-09-09

PRIOR APPLICATION NUMBER: PCT/IB01/00426

PRIOR FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: GB 0005585.5

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: GB 0015751.1

PRIOR FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 66

SOFTWARE: PatentIn version 3.0

SEQ ID NO 17

LENGTH: 213

TYPE: PRT

ORGANISM: Bacillus circulans

US-11-170-653-17

Query Match 99.7%; Score 1168; DB 7; Length 213;

Best Local Similarity 99.5%; Pred. No. 1.4e-95;

Matches 212; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFKEKKNFLVGLSAAALMSISLFSATASAASTDYQWQNTDGGGI VNAVNGSGNYSVNWSN 60

Db 1 MFKEKKNFLVGLSAAALMSISLFSATASAASTDYQWQNTDGGGI VNAVNGSGNYSVNWSN 60



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; SEQ ID NO 1
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-11-170-653-1
Query Match      88.9%; Score 1041; DB 7; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.5e-84; Indels 0; Gaps 0;
Matches 185; Conservative 0; Mismatches 0;

Qy 29 ASTDYQWQNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKWTGSPRTTINYNAGVWAP 88
Db 1 ASTDYQWQNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKWTGSPRTTINYNAGVWAP 60

Qy 89 NNGYLYLWTRSPLEIYYVVDWSGTYRPTGTYGTVKSDGGYDYITTTIRYNAPSIDG 148
Db 61 NNGYLYLWTRSPLEIYYVVDWSGTYRPTGTYGTVKSDGGYDYITTTIRYNAPSIDG 120

Qy 149 DRTTFTQVWSVROSKRPTGNSNATITFSNHNNAWKSHGMNLGSSNNAYQVMATEGYQSSGSS 208
Db 121 DRTTFTQVWSVROSKRPTGNSNATITFSNHNNAWKSHGMNLGSSNNAYQVMATEGYQSSGSS 180

Qy 209 NVTVM 213
Db 181 NVTVM 185

RESULT 8
US-10-517-939-198
; Sequence 198, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; PRIOR FILING DATE: 2004-12-13
; PRIOR FILING DATE: 2003-06-16
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
; NAME/KEY: SIGNAL
; LOCATION: (1)...(28)
US-10-517-939-198
Query Match      81.4%; Score 953; DB 6; Length 211;
Best Local Similarity 81.7%; Pred. No. 9e-77;
Matches 174; Conservative 13; Mismatches 24; Indels 2; Gaps 2;

Qy 1 MFKFKQFLVGLSAAALMSISLFSATASASTDYQWQNTDGGGIVNAVNGSGGNYSVNWSN 60
Db 1 MFKFSKQMTVLLAATMSFGLF-ATTSSAATDYQWQNTDGGGIVNAVNGSGGNYSVTQWQ 59

Qy 61 TGNFVVGKWTGSPRTTINYNAGVWAPNGNGYLYLWTRSPLEIYYVVDWSGTYRPTG 120
Db 60 TGNFVVGKWTGSPNRITINYNAGVWAPSGNGYLYLWTRNALIEIYYVVDWSGTYRPTG 119
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Qy 121 TYKGTAKSDGGTYDYITTTIRYNAPSIDGDRTTFTQVWSVROSKRPTGNSNATITFSNHVNA 180
Db 120 TYKGTVTSDGGTYDYITTTIRYNAPSIDGTO-TFAQYMSVROSKRATGVNSSITFSNHVNA 178

Qy 181 WKSHGMNLGSSNNAYQVMATEGYQSSGSSNVTVM 213
Db 179 WASKGMNLGSSWSYQVLATEGYQSSGSSNVTVM 211

RESULT 9
US-10-517-939-158
; Sequence 158, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 158
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
; NAME/KEY: SIGNAL
; LOCATION: (1)...(29)
US-10-517-939-158
Query Match      79.7%; Score 933.5; DB 6; Length 214;
Best Local Similarity 80.4%; Pred. No. 4.6e-75;
Matches 172; Conservative 12; Mismatches 29; Indels 1; Gaps 1;

Qy 1 MFKFKQFLVGLSAAALMS-ISLFSATASASTDYQWQNTDGGGIVNAVNGSGGNYSVNWS 59
Db 1 MFKLSKKILVLLTISMSFISLFAVTAASTDYQWQNTDGGGIVNAVNGSDGNYSVWS 60

Qy 60 NTGNFVVGKWTGSPRTTINYNAGVWAPNGNGYLYLWTRSPLEIYYVVDWSGTYRPT 119
Db 61 NCGNFVVGKWTGTSATRVINYNAGAFSPSGNGYLYLWTRNSLIEIYYVVDWSGTYRPT 120

Qy 120 GTYKGTAKSDGGTYDYITTTIRYNAPSIDGDRTTFTQVWSVROSKRPTGNSNATITFSNHVN 179
Db 121 GTYKGTVTSDGGTYDYITTTIRYNAPSIDGNNTFTQVWSVROSKRPIGNTITITFSNHVN 180

Qy 180 AWKSHGMNLGSSNNAYQVMATEGYQSSGSSNVTVM 213
Db 181 AWKSGMNLGSSWAYQVLATEGYQSSGSSNVTVM 214

RESULT 10
US-11-170-653-19
; Sequence 19, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sibbesen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
```



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; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170,653
; CURRENT FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 211
; TYPE: PRT
; ORGANISM: A. caviae
US-11-170-653-19

Query Match      79.3%; Score 929; DB 7; Length 211;
Best Local Similarity 79.3%; Pred. No. 1.le-74;
Matches 169; Conservative 18; Mismatches 24; Indels 2; Gaps 2;

Qy 1 MFKFKNPLVGLSAAALMSISLFSATASAASTDYQWNTDGGGIVNAVNGSGGNTSVNWSN 60
Db 1 MFKFKKMLTVVLAASMSFGVFAATSSAA-TDYQWNTDGGGIVNAVNGSGGNTSVNQW 59

Qy 61 TGNFVVGKGTGTPFRRTTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTG 120
Db 60 TGNFVVGKGTGTYGTPNRVYNYNAGVWAPNGNGYLTLYGWTRNALLIEYYVVDVSWGTYRPTG 119

Qy 121 TYGTVKSDGGTYDIYTTTRYNAPSIDGRTTFTQYWSVRQSKRPTGSGNATITFSNHVNA 180
Db 120 TYGTVNSDGGTYDIYTTTRYNAPSIDGTQ-TFQYWSVRQSKRPTGSGNATITFSNHVNA 178

Qy 181 WKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
Db 179 WPSKGMNLGSSWSYQVLATEGYQSSGSSNVTVW 211

RESULT 11
US-10-517-939-208
; Sequence 208, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 208
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(27)
US-10-517-939-208
```

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Query Match      79.2%; Score 927; DB 6; Length 210;
Best Local Similarity 80.1%; Pred. No. 1.7e-74;
Matches 169; Conservative 14; Mismatches 26; Indels 2; Gaps 2;

Qy 3 KFKKFNPLVGLSAAALMSISLFSATASAASTDYQWNTDGGGIVNAVNGSGGNTSVNWSNTG 62
Db 2 KLKKKMLTLLLTASMSFGLFGATSSAA-TDYQWNTDGGGIVNAVNGSGGNTSVTWQNSG 60

Qy 63 NFVVGKGTGTPFRRTTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTGTY 122
Db 61 NFVVGKGSVGSPPNRTTINYNAGIWEPSGNGYLTLYGWTRNALLIEYYVVDVSWGTYRPTGTH 120

Qy 123 KGTVKSDDGTYDIYTTTRYNAPSIDGRTTFTQYWSVRQSKRPTGSGNATITFSNHVNAWK 182
Db 121 KGTVNSDGGTYDIYTTTRYNAPSIDGTQ-TFQYWSVRQSKRPTGSGNATITFSNHVNAWR 179

Qy 183 SHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
Db 180 SKGMNLGSSWSYQVLATEGYQSSGSSNVTVW 210

RESULT 12
US-11-170-653-18
; Sequence 18, Application US/11170653
; Publication No. US20050271769A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sibbesen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/11/170,653
; CURRENT FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Bacillus stearotheophilus
US-11-170-653-18

Query Match      77.5%; Score 907.5; DB 7; Length 211;
Best Local Similarity 79.2%; Pred. No. 8.6e-73;
Matches 168; Conservative 12; Mismatches 29; Indels 3; Gaps 3;

Qy 3 KFKKFNPLVGLSAAALMSISLFSATASAASTDYQWNTDGGGIVNAVNGSGGNTSVNWSNTG 62
Db 2 KLKKKMLTLLLTASMSFGLFGATSSAA-TDYQWNTDGGGIVNAVNGSGGNTSVTWQNTG 60

Qy 63 NFVVGKGTGTPFRRTTINYNAGVWAPNGNGYLTLYGWTRSPLEIYYVVDVSWGTYRPTGTY 122
Db 61 NFVVGKGTGTPFRRTTINYNAGIWEPSGNGYLTLYGWTRNALLIEYYVVDVSWGTYRATGNY 120

Qy 123 K-GTVKSDGGTYDIYTTTRYNAPSIDGRTTFTQYWSVRQSKRPTGSGNATITFSNHVNAW 181
Db 121 ESGTVNSDGGTYDIYTTTRYNAPSIDGTQ-TFQYWSVRQSKRPTGSGNATITFSNHVNAW 179

Qy 182 KSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW 213
Db 180 RSKGMNLGSSWAYQVLATEGYQSSGSSNVTVW 211

RESULT 13
US-10-517-939-190
```

```
; Sequence 190, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 190
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
; US-10-517-939-190

Query Match 75.7%; Score 886; DB 6; Length 189;
Best Local Similarity 84.0%; Pred. No. 5.8e-71;
Matches 158; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

Qy 26 ASAASTDYQWNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTTINYNAGV 85
Db 2 ALMASTDYQWNTDGGGIVNAVNGSGGNYSVNWSNCGNFVVGKGTGSTRVINYAGA 61

Qy 86 WAPNGNGYLTYGWTRSPLEIYYVVDVSMGTYPRTGTYKGTGSDGTYDIYTTTNYAPS 145
Db 62 FSPSGNGYALYLGWTRNSLIEYYVVDVSMGTYPRTGTYKGTGSDGTYDIYTTTNYAPS 121

Qy 146 IDGRTTFTQWVSQRKPTGSGNATITFSNHVNAWKGHNLGNNWAYQVMATEGYQSS 205
Db 122 IDGNNTTFTQWVSQRKRPITGNTTITFSNHVNAWKGHNLGSSWSYQVLATEGYQSS 181

Qy 206 GSSNVTVW 213
Db 182 GYSNVTVW 189

RESULT 14
US-10-517-939-252
; Sequence 252, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; US-10-517-939-252
```

```
; SEQ ID NO 252
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
; US-10-517-939-252

Query Match 74.6%; Score 873.5; DB 6; Length 184;
Best Local Similarity 83.2%; Pred. No. 7e-70;
Matches 153; Conservative 15; Mismatches 15; Indels 1; Gaps 1;

Qy 30 STDYQWNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTTINYNAGVWAPN 89
Db 2 ATDYQWNTDGGGIVNAVNGSGGNYSVTWQNSGDFVVGKGSVSPNRTTINYNAGIWEPS 61

Qy 90 GNGYLTLYGWTRSPLEIYYVVDVSMGTYPRTGTYKGTGSDGTYDIYTTTNYAPSIDGD 149
Db 62 GNGYLTLYGWTRNSLIEYYVVDVSMGTYPRTGTHKGTVNSDGTVDIYTTMYNAPSIDGT 121

Qy 150 RTTFTQWVSQRKPTGSGNATITFSNHVNAWKGHNLGNNWAYQVMATEGYQSSGSSN 209
Db 122 Q-TFQQFWSVRQSKRPTGSGNVSITFSNHVNAWRKGMNLGSSWSYQVLATEGYQSSGRSN 180

Qy 210 VTVW 213
Db 181 VTVW 184

RESULT 15
US-10-517-939-380
; Sequence 380, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghlalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 380
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated polypeptide.
; US-10-517-939-380

Query Match 72.1%; Score 844; DB 6; Length 189;
Best Local Similarity 81.4%; Pred. No. 2.8e-67;
Matches 153; Conservative 10; Mismatches 25; Indels 0; Gaps 0;

Qy 26 ASAASTDYQWNTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGTGSPRTTINYNAGV 85
Db 2 ALMASTFYWHNTDGGIVNAVNGSDGNYSVSWNCGNFVVGKGTGSTRVINYAHA 61

Qy 86 WAPNGNGYLTYGWTRSPLEIYYVVDVSMGTYPRTGTYKGTGSDGTYDIYTTTNYAPS 145
Db 62 FSPVGNAYLALYLGWTRNSLIEYYVVDVSMGTYPRTGTYKGTGSDGTYDIYTTTNYAPS 121

Qy 146 IDGRTTFTQWVSQRKPTGSGNATITFSNHVNAWKGHNLGNNWAYQVMATEGYQSS 205
```

Db 122 IDGNITTFQFWSVRQSKRPICGTNNTITFSNHNVAWKSCKGNLGSWSYQVLATEGYQSS 181

Qy 206 GSSNVTW 213

Db 182 GYSNVTW 189

Search completed: February 3, 2006, 09:24:52  
Job time : 11 secs

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